

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 28, 2006, 18:18:07 ; Search time 151 Seconds
(without alignments)
2713.727 Million cell updates/sec

Profile: US-10-726-093-10

Perfect score: 758
Sequence: 1 MENELFCGSLVHPQWVLSA.....SRGLTQSSASQAECPLCCSA 146

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1 COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq:*
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- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCUTS COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	758	100.0	1265	3	US-09-020-956-173 Sequence 173, App
2	758	100.0	1265	3	US-09-030-607-173 Sequence 173, App
3	758	100.0	1265	3	US-09-439-313-173 Sequence 173, App
4	758	100.0	1265	3	US-09-352-616A-173 Sequence 173, App
5	758	100.0	1265	3	US-09-232-149A-173 Sequence 173, App
6	758	100.0	1265	3	US-09-159-812-173 Sequence 173, App
7	758	100.0	1265	3	US-09-636-215-173 Sequence 173, App
8	758	100.0	1265	3	US-09-685-166A-173 Sequence 173, App

9	758	100.0	1265	3	US-09-115-453-173 Sequence 173, App
10	758	100.0	1265	3	US-09-688-489-173 Sequence 173, App
11	758	100.0	1265	3	US-09-679-426-173 Sequence 173, App
12	758	100.0	1265	3	US-09-759-143-173 Sequence 173, App
13	758	100.0	1265	3	US-09-651-236-173 Sequence 173, App
14	758	100.0	1265	3	US-09-030-606-173 Sequence 173, App
15	758	100.0	1265	3	US-09-657-279-173 Sequence 173, App
16	758	100.0	1265	3	US-10-012-896-173 Sequence 173, App
17	758	100.0	1265	5	US-09-116-134-173 Sequence 173, App
18	758	100.0	1265	5	US-10-144-678A-173 Sequence 173, App
19	695	91.7	484	3	US-09-621-976-277 Sequence 177, App
20	660	87.1	4740	5	US-09-936-271C-1 Sequence 1, Appl1
21	640	84.4	1459	3	US-09-020-956-174 Sequence 174, App
22	640	84.4	1459	3	US-09-439-313-174 Sequence 174, App
23	640	84.4	1459	3	US-09-352-616A-174 Sequence 174, App
24	640	84.4	1459	3	US-09-233-149A-174 Sequence 174, App
25	640	84.4	1459	3	US-09-159-812-174 Sequence 174, App
26	640	84.4	1459	3	US-09-636-215-174 Sequence 174, App
27	640	84.4	1459	3	US-09-685-166A-174 Sequence 174, App
28	640	84.4	1459	3	US-09-115-453-174 Sequence 174, App
29	640	84.4	1459	3	US-09-688-489-174 Sequence 174, App
30	640	84.4	1459	3	US-09-679-426-174 Sequence 174, App
31	640	84.4	1459	3	US-09-759-143-174 Sequence 174, App
32	640	84.4	1459	3	US-09-651-236-174 Sequence 174, App
33	640	84.4	1459	3	US-09-030-606-174 Sequence 174, App
34	640	84.4	1459	3	US-09-657-279-174 Sequence 174, App
35	640	84.4	1459	3	US-10-012-896-174 Sequence 174, App
36	640	84.4	1459	5	US-10-116-134-174 Sequence 174, App
37	640	84.4	1459	5	US-10-144-678A-174 Sequence 174, App
38	589	77.7	396	3	US-09-621-976-1662 Sequence 1662, Ap
39	589	77.7	765	3	US-09-439-313-524 Sequence 524, App
40	588	77.6	765	3	US-09-636-215-524 Sequence 524, App
41	588	77.6	765	3	US-09-685-166A-524 Sequence 524, App
42	588	77.6	765	3	US-09-679-426-524 Sequence 524, App
43	588	77.6	765	3	US-09-759-143-524 Sequence 524, App
44	588	77.6	765	3	US-09-651-236-524 Sequence 524, App
45	588	77.6	765	3	US-09-651-236-524 Sequence 524, App

ALIGNMENTS

RESULT 1
US-09-020-956-173
Sequence 173, Application US/09020956
Patent No. 6261362
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS F
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020.956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 1265 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-020-956-173

Alignment Scores:
Pred. No.: 4,3e-79 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-020-956-173 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAACGAATGTTCTGCTCGGCGCTGCTGTCATCCGACGTGGTCTGTCAGCC 99

QY 21 AlaHisCysPheGlnAsnSerGlyThrIleGlyLeuGlyLeuHisSerLeuGlnAlaAsp 40
DB 100 GCACACTGTTCCAGAACTCTACACATCGGGCTGGCTGCAGACACTTTCAGGGCCGAC 159

QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpValAsn 60
DB 160 CAAGAGCCAGGAGCGAGATGTGTGAGGCGAGCTCTCCGTACGGACCCAGAGTACAC 219

QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGlnSer 80
DB 220 AGACCTTCTGCTGCTAACGACCTCATGCTCATTAAGTTGACGAACTCCGTCCAGTCT 279

QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGCATGACATGCTTCGACATGCCCTACCGGGGAACTTTCCTCCTC 339

QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValLysLeuProSerSer 120
DB 340 GTTTCGCTGGGCTGCTGCTGCGAAGCGGAGCTACGGGTGTGTCTGCTCTTCA 399

QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlnCys 140
DB 400 AGAAGGTCTCTGCTGACGATCGCGGGGCTGACCCAGACTCTGCTCCAGGAGAAATGC 459

QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCGAGTGGC 477

RESULT 2
US-09-030-607-173
Sequence 173, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 1265 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-607-173

Alignment Scores:
Pred. No.: 4,3e-79 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-030-607-173 (1-1265)

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DB 40 ATGGAAACGAATGTTCTGCTCGGCGCTGCTGTCATCCGACGTGGTCTGTCAGCC 99

QY 21 AlaHisCysPheGlnAsnSerGlyThrIleGlyLeuGlyLeuHisSerLeuGlnAlaAsp 40
DB 100 GCACACTGTTCCAGAACTCTACACATCGGGCTGGCTGCAGACACTTTCAGGGCCGAC 159

QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpValAsn 60
DB 160 CAAGAGCCAGGAGCGAGATGTGTGAGGCGAGCTCTCCGTACGGACCCAGAGTACAC 219

QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGlnSer 80
DB 220 AGACCTTCTGCTGCTAACGACCTCATGCTCATTAAGTTGAGACGAATCCGTGCCAGTCT 279

QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGCATGACATGCTTCGACATGCCCTACCGGGGAACTTTCCTCCTC 339

QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValLysLeuProSerSer 120
DB 340 GTTTCGCTGGGCTGCTGCTGCGAAGCGGAGCTACGGGTGTGTCTGCTCTTCA 399

QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlnCys 140
DB 400 AGAAGGTCTCTGCTGACGATCGCGGGGCTGACCCAGACTCTGCTCCAGGAGAAATGC 459

QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCGAGTGGC 477

RESULT 3
US-09-439-313-173
Sequence 173, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.

```

; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 173
; LENGTH: 1265
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1265)
; OTHER INFORMATION: n = A,T,C or G
; US-09-439-313-173

Alignment Scores:
Pred. No.: 4.3e-79 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

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DB 40 ATGGAAAGCAATTTGCTGCTCGGGGCTCTGTCATCCGAGTGGGTGTAGCC 99
QY 21 AlaHisCySPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACTCTTACACCATGGGGCTGGCCCTTGAGCCGAC 159
QY 41 GlnGluProGlySergInMeValGluAlaSerLeuSerValArgHisProGluTyAsn 60
DB 160 CAAGAGCCAGGAGCCAGATGTGAGGAGCCAGCTCCGTAAGGACCCAGAGTACAAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleYsLeuAspGluSerValSergIuser 80
DB 220 AGACCTTGTCTCTCAACGACCTCATGCTCATCAAGTTGAGCAATCCGTCCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGACATCAGATTGCTTCCAGTGCCTTACCGGGGAATCTTGCCTC 339
QY 101 ValSergIlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTTTGGCTGGGGTGTGCTGGGCAAGGTGAGCTCAAGGTGTGTGTGCTGCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGAGAGTCTCTTCCGCGGAGTGGGCTGACCAAGAGCTGTGCTCCAGGAGAAATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCAAGTGC 477

RESULT 4
US-09-352-616A-173
; Sequence 173, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.

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; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 173
; LENGTH: 1265
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1265)
; OTHER INFORMATION: n = A,T,C or G
; US-09-352-616A-173

Alignment Scores:
Pred. No.: 4.3e-79 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

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QY 21 AlaHisCySPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACTCTTACACCATGGGGCTGGCCCTTGAGCCGAC 159
QY 41 GlnGluProGlySergInMeValGluAlaSerLeuSerValArgHisProGluTyAsn 60
DB 160 CAAGAGCCAGGAGCCAGATGTGAGGAGCCAGCTCCGTAAGGACCCAGAGTACAAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleYsLeuAspGluSerValSergIuser 80
DB 220 AACCTTGTCTCTCAACGACCTCATGCTCATCAAGTTGAGCAATCCGTCCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGACATCAGATTGCTTCCAGTGCCTTACCGGGGAATCTTGCCTC 339
QY 101 ValSergIlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTTTGGCTGGGGTGTGCTGGGCAAGGTGAGCTCAAGGTGTGTGTGCTGCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGAGAGTCTCTTCCGCGGAGTGGGCTGACCAAGAGCTGTGCTCCAGGAGAAATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCAAGTGC 477

RESULT 5
US-09-232-149A-173
; Sequence 173, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

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FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232.149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 173
LENGTH: 1265
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1265)
OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-173
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Alignment Scores:

Pred. No.:	4.3e-79	Length:	1265
Score:	758.00	Matches:	146
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-726-093-10 (1-146) x US-09-232-149A-173 (1-1265)

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QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGAAACGAAATTGTTCTGCTCGGGCGTCTGTGTCATCCGACAGGGGTGCTGTACAGCC 99
QY 21 AlaHisCysPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACTCTTACACATCGGGGCTGGGCTTCCACAGTCTTGAAGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpValAsn 60
DB 160 CAAAGCCAGGAGACCGAGATGTGTGAGAGGCCAGCTCTCCGTACGGACCCACAGATACAAAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGTCTGCTGATACGACCTCATGCTCAAGTTGAGCAATCCGTGTCCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGATGATCGCATGTGTCGACAGTCCCTTACCGCGGGAACCTTGTGCTTC 339
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyLeuLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGCTGGGGTGTGCTGTGGGAAAGGTGAGCTCACGGGTGTGTGTGCTGCTCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgIleGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGGAGGTCTCTGCTCCAGTCGCGGGGGGTGACCCAGAGCTTGTGCTGCCAGCAGATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCAAGTGC 477
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RESULT 6

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US-09-159-812-173
Sequence 173, Application US/09159812A
Patent No. 6613872
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.428C5
CURRENT APPLICATION NUMBER: US/09/159.812A
CURRENT FILING DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 306
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 173
LENGTH: 1265
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TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1265)
OTHER INFORMATION: n = A,T,C or G
US-09-159-812-173
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Alignment Scores:

Pred. No.:	4.3e-79	Length:	1265
Score:	758.00	Matches:	146
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

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QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGAAACGAAATTGTTCTGCTCGGGCGTCTGTGTCATCCGACAGGGGTGCTGTACAGCC 99
QY 21 AlaHisCysPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACTCTTACACATCGGGGCTGGGCTTCCACAGTCTTGAAGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpValAsn 60
DB 160 CAAAGCCAGGAGACCGAGATGTGTGAGAGGCCAGCTCTCCGTACGGACCCACAGATACAAAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGTCTGCTGATACGACCTCATGCTCAAGTTGAGCAATCCGTGTCCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGATGATCGCATGTGTCGACAGTCCCTTACCGCGGGAACCTTGTGCTTC 339
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyLeuLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGCTGGGGTGTGCTGTGGGAAAGGTGAGCTCACGGGTGTGTGTGCTGCTCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgIleGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGGAGGTCTCTGCTCCAGTCGCGGGGGGTGACCCAGAGCTTGTGCTGCCAGCAGATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCAAGTGC 477
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RESULT 7

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US-09-636-215-173
Sequence 173, Application US/09636215
Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
```

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121.42717C17
 CURRENT APPLICATION NUMBER: US/09/636,215
 CURRENT FILING DATE: 2000-08-10
 NUMBER OF SEQ ID NOS: 852
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 173
 LENGTH: 1265
 TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)...(1265)
 OTHER INFORMATION: n = A,T,C or G
 US-09-636-215-173

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
4,3e-79	758.00	1265	146	0	0	0	0
Percent Similarity:	100.0%						
Best Local Similarity:	100.0%						
Query Match:	100.0%						

US-10-726-093-10 (1-146) x US-09-636-215-173 (1-1265)

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QY      1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB      40 ATGGAAAAGCAATTGTTCTGCTCGGCGCTCTGTCATCCGACAGGGGTGCTGACGCC 99
QY      21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaasp 40
DB      100 GCACACTGTTTCCAGAACTCTACACCATCGGGCTGGCTGCACAGCTTTGAGGCCGAC 159
QY      41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60
DB      160 CAAGAGCCAGGAGGCGCAGATGTGTGAGGCGCAGCTCTCGTACGACGCCAGGTCACAC 219
QY      61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB      220 AGACCTTGCTGCTCAACACCTCACTGCTCATCAATTGGACGAATCCGGTCCGAGTCT 279
QY      81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB      280 GACACCATCCGAGGAGCATGAGATTGCTTCGACAGTCCCTACCCGGGGAACTTTCCTC 339
QY      101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB      340 GTTTCGGCTGGGGTCTGCTGGGGAACGCTGAGCTCAAGGGTGTGTGCTGCTTCA 399
QY      121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB      400 AGGAGGTCTCTGCTCCAGTCCGAGGCGGCTGACCCAGAGCTCTGCTCCAGGAGATGC 459
QY      141 LeuProCysCysSerAla 146
DB      460 CTACCGTCTGCAGTGCG 477

```

RESULT 8

US-09-685-166A-173
 Sequence 173, Application US/09685166A
 Patent No. 6630305
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yugu
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Aijun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121.427C21
 CURRENT APPLICATION NUMBER: US/09/685,166A
 CURRENT FILING DATE: 2000-10-10
 NUMBER OF SEQ ID NOS: 898
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 173
 LENGTH: 1265
 TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)...(1265)
 OTHER INFORMATION: n = A,T,C or G
 US-09-685-166A-173

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
4,3e-79	758.00	1265	146	0	0	0	0
Percent Similarity:	100.0%						
Best Local Similarity:	100.0%						
Query Match:	100.0%						

US-10-726-093-10 (1-146) x US-09-685-166A-173 (1-1265)

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QY      1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB      40 ATGGAAAAGCAATTGTTCTGCTCGGCGCTCTGTCATCCGACAGGGGTGCTGACGCC 99
QY      21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaasp 40
DB      100 GCACACTGTTTCCAGAACTCTACACCATCGGGCTGGCTGCACAGCTTTGAGGCCGAC 159
QY      41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60
DB      160 CAAGAGCCAGGAGGCGCAGATGTGTGAGGCGCAGCTCTCGTACGACGCCAGGTCACAC 219
QY      61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB      220 AGACCTTGCTGCTCAACACCTCACTGCTCATCAATTGGACGAATCCGGTCCGAGTCT 279
QY      81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB      280 GACACCATCCGAGGAGCATGAGATTGCTTCGACAGTCCCTACCCGGGGAACTTTCCTC 339
QY      101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB      340 GTTTCGGCTGGGGTCTGCTGGGGAACGCTGAGCTCAAGGGTGTGTGCTGCTTCA 399
QY      121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB      400 AGGAGGTCTCTGCTCCAGTCCGAGGCGGCTGACCCAGAGCTCTGCTCCAGGAGATGC 459
QY      141 LeuProCysCysSerAla 146
DB      460 CTACCGTCTGCAGTGCG 477

```

RESULT 9

US-09-115-453-173
 Sequence 173, Application US/09115453B
 Patent No. 6657056
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.

```

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 173
; LENGTH: 1265
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1265)
; OTHER INFORMATION: n = A,T,C or G
US-09-115-453-173

Alignment Scores:
Pred. No.: 4,3e-79 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-115-453-173 (1-1265)
QY 1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAAACGAATTTCTGCTCGGCGCTCGTGCATCCGACATGGGTGCTGCACCC 99
QY 21 AlaHisCysPheGlnAsnSerTyrrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACCTTCAACCTCAGCCATCGGGCTGCGACAGTCTGAGGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyrAsn 60
DB 160 CAAGAGCCAGGAGCCAGATGTGTGAGGCCAGCTCTCCGTAAGCCAGACCCAGATACAA 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleTyrLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGTCTGCTTAACGACTTCACTCATGCTCAAGATCCGTTCCGAGTCT 279
QY 81 AsprThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGACATGACGATCTTCTCGCAGTCCCTTACCGCGGGAACCTTGCCTC 339
QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTTCGTGGGTGGGTCTGCTGCGAAGCGGTGAGCTCAGCGGTGTGTCTGCTCCCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGGAGCTCTCTGCGCCAGTCGCGGGGGGTGACCCAGAGCTGCTCCAGGACAGATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTGTGCAAGTGC 477

RESULT 10
US-09-688-489-173
; Sequence 173, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
```

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; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 173
; LENGTH: 1265
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1265)
; OTHER INFORMATION: n = A,T,C or G
US-09-688-489-173

Alignment Scores:
Pred. No.: 4,3e-79 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-688-489-173 (1-1265)
QY 1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAAACGAATTTCTGCTCGGCGCTCGTGCATCCGACATGGGTGCTGCACCC 99
QY 21 AlaHisCysPheGlnAsnSerTyrrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACCTTCAACCTCAGCCATCGGGCTGCGACAGTCTGAGGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyrAsn 60
DB 160 CAAGAGCCAGGAGCCAGATGTGTGAGGCCAGCTCTCCGTAAGCCAGACCCAGATACAA 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleTyrLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGTCTGCTTAACGACTTCACTCATGCTCAAGTGAACGATCGTTCGAGTCT 279
QY 81 AsprThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGACATGACGATTTCTTCCAGTGCCTTACCGGGGGAACCTTGCCTC 339
QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTTCGTGGGTGGGTCTGCTGCGAAGCGGTGAGCTCAGCGGTGTGTCTGCTCCCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGGAGCTCTCTGCGCCAGTCGCGGGGGGTGACCCAGAGCTTGTGCTCCAGGACAGATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTGTGCAAGTGC 477

RESULT 11
US-09-679-426-173
; Sequence 173, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
```

APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121.427C20
 CURRENT APPLICATION NUMBER: US/09/679,426
 CURRENT FILING DATE: 2000-10-02
 NUMBER OF SEQ ID NOS: 895
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 173
 LENGTH: 1265
 TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)...(1265)
 OTHER INFORMATION: n = A,T,C or G
 US-09-679-426-173

Alignment Scores:
 Pred. No.: 4.3e-79 Length: 1265
 Score: 758.00 Matches: 146
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 Gaps: 0
 DB: 3

US-10-726-093-10 (1-146) x US-09-679-426-173 (1-1265)

QY 1 MetGluAaNGluLeuPheCySerGlyValLeuValHisProGlnTrpValLeuSerAla 20
 DB 40 ATGAAACGAATGTTCTGCTCGGCGCTCTGTCGTCATCCGCAATGGGTCTGTCAACC 99
 QY 21 AlaHisCySPheGlnAaNSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaASP 40
 DB 100 GCACACTGTCTTCCAAACTCTTACACCACTCGGCTGGGCTGTCACAGCTTGAGCCAC 159
 QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyrAsn 60
 DB 160 CAAGAGCCAGGAGCAGATGTTGAGGCGACCTCTCGTACGGCACCAGATACAAAC 219
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
 DB 220 AGACCTTGTCTGCTACACCACTCTCATCAAGTTGAGCAATCGGTGTCGAGTCT 279
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCySProThrAlaGlyAsnSerCysLeu 100
 DB 280 GACACCATCCGAGAGATCGCATGCTTGCAGTGCCCTTACCGCGGGAACCTTGCCCTC 339
 QY 101 ValSerGlyTTPGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
 DB 340 GTTCTGTGCTGGGCTGTGCTGCGAAGCGTCAAGGCTGAGGCTGCTGCTGCTCTTCA 399
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
 DB 400 AGAGAGTCTCTGCGCAGTCGGGGGCGGAGCCAGACGCTGCGTCCAGAGAGATGC 459
 QY 141 LeuProCyCySerAla 146
 DB 460 CTACCGTCTGCAGTGGC 477

RESULT 12
 US-09-759-143-173
 Sequence 173, Application US/09759143

GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Devin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yugu
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Aijun
 APPLICANT: Skeiky, Yasir A.W.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121.427C23
 CURRENT APPLICATION NUMBER: US/09/759,143
 CURRENT FILING DATE: 2001-01-12
 NUMBER OF SEQ ID NOS: 934
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 173
 LENGTH: 1265
 TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)...(1265)
 OTHER INFORMATION: n = A,T,C or G
 US-09-759-143-173

Alignment Scores:
 Pred. No.: 4.3e-79 Length: 1265
 Score: 758.00 Matches: 146
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 Gaps: 0
 DB: 3

US-10-726-093-10 (1-146) x US-09-759-143-173 (1-1265)

QY 1 MetGluAaNGluLeuPheCySerGlyValLeuValHisProGlnTrpValLeuSerAla 20
 DB 40 ATGAAACGAATGTTCTGCTCGGCGCTCTGTCGTCATCCGCAATGGGTCTGTCAACC 99
 QY 21 AlaHisCySPheGlnAaNSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaASP 40
 DB 100 GCACACTGTCTTCCAAACTCTTACACCACTCGGCTGGGCTGTCACAGCTTGAGCCAC 159
 QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyrAsn 60
 DB 160 CAAGAGCCAGGAGCAGATGTTGAGGCGACCTCTCGTACGGCACCAGATACAAAC 219
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
 DB 220 AGACCTTGTCTGCTACACCACTCTCATCAAGTTGAGCAATCGGTGTCGAGTCT 279
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCySProThrAlaGlyAsnSerCysLeu 100
 DB 280 GACACCATCCGAGAGATCGCATGCTTGCAGTGCCCTTACCGCGGGAACCTTGCCCTC 339
 QY 101 ValSerGlyTTPGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
 DB 340 GTTCTGTGCTGGGCTGTGCTGCGAAGCGTCAAGGCTGAGGCTGCTGCTGCTCTTCA 399
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
 DB 400 AGAGAGTCTCTGCGCAGTCGGGGGCGGAGCCAGACGCTGCGTCCAGAGAGATGC 459
 QY 141 LeuProCyCySerAla 146
 DB 460 CTACCGTCTGCAGTGGC 477

RESULT 13
 US-09-651-236-173
 Sequence 173, Application US/09651236
 Patent No. 6818751

```
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqi
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Hepler, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.42718C18
/ CURRENT APPLICATION NUMBER: US/09/651.236
/ NUMBER OF SEQ ID NOS: 865
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 173
/ LENGTH: 1265
/ TYPE: DNA
/ ORGANISM: Homo sapien
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(1265)
/ OTHER INFORMATION: n = A,T,C or G
US-09-651-236-173

Alignment Scores:
Pred. No.: 4.3e-79 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-651-236-173 (1-1265)
QY 1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAGAAAGCAATTGTTCTGCTGGGCGTCTGTCATCCGAGTGGGTGCTGTACGCC 99
QY 21 AlaHisCysPheGlnAAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACGTTTCCAGAACTCCTACACCATCGGGCTGGCGACAGTCTTGAGGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpAsn 60
DB 160 CAAGAGCCAGGAGGAGCAGATGGTGAGGCCAGCCTCTCCCTACGCGACCCAGAGTACAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGTGCTGCTACGACCTATGCTCATCAAGTTGAGCAAGATCCGTGTCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCCATCCGAGACATCAGCATGCTTCCAGAGTCCGCGGAGAACTTGTGCTCT 339
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTTCGTGGGTGGGTGTGCTGGCGAAGCGTGAGCTCAGGGGTGTGTCTGCTCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 459
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QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCTGAGTGCG 477

RESULT 14
US-09-030-606-173
/ Sequence 173, Application US/09030606
/ Patent No. 6887660
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS
/ NUMBER OF SEQUENCES: 224
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ City: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/030,606
/ FILING DATE: 25-FEB-1998
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Waki, David J.
/ REGISTRATION NUMBER: 31,392
/ REFERENCE/DOCKET NUMBER: 210121.428C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 173:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1265 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
US-09-030-606-173

Alignment Scores:
Pred. No.: 4.3e-79 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-030-606-173 (1-1265)
QY 1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAGAAAGCAATTGTTCTGCTGGGCGTCTGTCATCCGAGTGGGTGCTGTACGCC 99
QY 21 AlaHisCysPheGlnAAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACGTTTCCAGAACTCCTACACCATCGGGCTGGCGACAGTCTTGAGGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpAsn 60
DB 160 CAAGAGCCAGGAGGAGCAGATGGTGAGGCCAGCCTCTCCCTACGCGACCCAGAGTACAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGTGCTGCTACGACCTATGCTCATCAAGTTGAGCAAGATCCGTGTCGAGTCT 279
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QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGGAGCATCAGCATGCTTCCAGAGCCCTACCGGGGAACTCTTGCTC 339
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGlnLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGCTGGGGGTCTGCTGGCGACGAGCTCAGGGGTGTGTCTGCTCTTCA 399
QY 121 ArgArgSerSerIleArgIleLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGAGAGTCTCTGCTGCCAGTCCGGGGGCTACCAAGCTCTGCTCCAGGCGAATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCAGTGG 477

RESULT 15.
US-09-657-279-173
; Sequence 173, Application US/09657279
; Patent No. 6894146
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqun
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kaios, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C19
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 877
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 173
; LENGTH: 1265
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1265)
; OTHER INFORMATION: n = A,T,C or G
US-09-657-279-173

Alignment Scores:
Pred. No.: 4,3e-79 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-657-279-173 (1-1265)
QY 1 MetGluAsnGlnLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAACGAATGTTCTGCTGGGGCTGTCGATCCGAGTGGGTGCTGTCAGCC 99
QY 21 AlaHisCysPheGlnAsnSerTrpThrIleGlyLeuGlyLeuHisSerLeuGlnAlaAsp 40
DB 100 GCACACTGTTCCAGAACTCTACACATCGGGCTGGGCTTGCACTTTAGGCGGAC 159
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QY 41 GlnGluProGlySerGlnMetValGlnAlaSerLeuSerValArgHisProGlnTrpAsn 60
DB 160 CAAAGCCAGGAGCCAGATGTGTGAGGCGCAGCTCTCCGTAGGCAACCAAGTCAAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGlnSerValSerGlnSer 80
DB 220 AGACCTTGCTCGCTAACGACCTCATGCTCATCAAGTTGACGAATCCGTGTGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGGAGCATCAGCATGCTTCCAGAGCCCTACCGGGGAACTCTTGCTC 339
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGlnLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGCTGGGGGTCTGCTGGCGAAGCTCAGGGGTGTGTCTGCTCTTCA 399
QY 121 ArgArgSerSerIleArgIleLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGAGAGTCTCTGCTGCCAGTCCGGGGGCTACCAAGCTCTGCTCCAGGCGAATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCAGTGG 477
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Search completed: August 28, 2006, 18:28:06
Job time : 152 secs

US-10-726-093-3

Alignment Scores:
Pred. No.: 1,35e-87 Length: 702
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-726-093-10 (1-146) x US-10-726-093-3 (1-702)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 1 ATGGAAGAAAGAAATGTTCTGCTCGGCGCTCTGCTGATCCGACAGTGGTCTGTACAGCC 60
QY 21 AlaHisCysPheGlnAsnSerTyrrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 61 GCACACTGTTCCAGAACTCTTACACCATCGGGCTGGCTGCACAGTCTTGAGGCCGAC 120
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpAsn 60
DB 121 CAAGAGCCAGGAGCCAGATGTGGAGGCCAGCTCTCCGTACGACCCAGATGACAC 180
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 181 AGACCTTCTCGCTTACACCATCGCTCATCAAGTTGACGAAATCCGTGCCAGTCT 240
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 241 GACACCATCCGAGATGATGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 301 GTTTCGGCTGGGGTCTGCTGCGAAGCGTGAAGCTTACGGGTGTGTCTGCTGCTTCA 360
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 361 AGAGAGTCTCTGCTGCCAGTCCGGGGCTGACCCAGAGCTCTGCTGCCAGGAGAAATGC 420
QY 141 LeuProCysCysSerAla 146
DB 421 CTACCGTCTGCTGCAGTCCG 438

RESULT 2

US-10-473-485-1

/ Sequence 1, Application US/10473485
/ Publication No. US20040137455A1
/ GENERAL INFORMATION:
/ APPLICANT: Clements, Judith A
/ APPLICANT: Dong, Ying
/ TITLE OF INVENTION: Polynucleotides and polypeptides linked to cancer and/or benign
/ FILE REFERENCE: DAV1172.004APC
/ CURRENT FILING DATE: 2003-09-29
/ PRIOR APPLICATION NUMBER: US/10/473,485
/ PRIOR FILING DATE: 2001-03-27
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 848
/ TYPE: DNA
/ ORGANISM: human
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(585)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: 3'UTR
/ LOCATION: (586)..(847)
/ OTHER INFORMATION:
US-10-473-485-1

Alignment Scores:

Pred. No.: 1,75e-87 Length: 848
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-726-093-10 (1-146) x US-10-473-485-1 (1-848)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 148 ATGGAAGAAAGAAATGTTCTGCTCGGCGCTCTGCTGATCCGACAGTGGTCTGTACAGCC 207
QY 21 AlaHisCysPheGlnAsnSerTyrrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 208 GCACACTGTTCCAGAACTCTTACACCATCGGGCTGGCTGCACAGTCTTGAGGCCGAC 267
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpAsn 60
DB 268 CAAGAGCCAGGAGCCAGATGTGGAGGCCAGCTCTCCGTACGACCCAGATGACAC 327
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 328 AGACCTTCTCGCTTACACCATCGCTCATCAAGTTGACGAAATCCGTGCCAGTCT 387
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 388 GACACCATCCGAGATGATGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 447
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 448 GTTTCGGCTGGGGTCTGCTGCGAAGCGTGAAGCTTACGGGTGTGTCTGCTGCTTCA 507
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 508 AGAGAGTCTCTGCTGCCAGTCCGGGGCTGACCCAGAGCTCTGCTGCCAGGAGAAATGC 567
QY 141 LeuProCysCysSerAla 146
DB 568 CTACCGTCTGCTGCAGTCCG 585

RESULT 3

US-09-759-143-173

/ Sequence 173, Application US/09759143
/ Patent No. US20020022248A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqun
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yael A.W.
/ APPLICANT: Hepler, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.427C23
/ CURRENT APPLICATION NUMBER: US/09/759,143
/ CURRENT FILING DATE: 2001-01-12
/ NUMBER OF SEQ ID NOS: 934
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 173
/ LENGTH: 1265

TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1265)
OTHER INFORMATION: n = A,T,C or G
US-09-759-143-173

Alignment Scores:
Pred. No.: 3,05e-87 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-759-143-173 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAAGCAATTTCTTCTGCTGGGCGCTCTGTCATCCGACAGTGGTGTGAGCC 99
QY 21 AlaHisCysPheGlnAsnSerTrpThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCAGAACTCTACACCATCGGCTGGGCTGCAACAGCTTGAAGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTrpAsn 60
DB 160 CAAGACCCAGGAGCCAGATGTTGAGAGCCAGCTCTCCGTACAGGACCCAGAGTCAAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTCTGCTCTCAACGACCTCATGCTCATCAAGTTGACCAATCCGTCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACATCCGAGGACCATGCTTCCAGATGCCCTTACCCGGGGAACCTTTCCTC 339
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGCTGGGGGTCTGCTGGGGAACGAGTCAAGGTCGTGCTGCTCTTCA 399
QY 121 ArgArgSerSerIleGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGGAGGTCTCTCTCCGACCTGCGGGGCTGACCCAGAGCTCTGCTCCAGGAGAAATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTGTGACAGTGC 477

RESULT 4
US-09-780-669-173

Sequence 173, Application US/09780669
Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Uiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John

APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780.669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 173
LENGTH: 1265
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1265)
OTHER INFORMATION: n = A,T,C or G
US-09-780-669-173

Alignment Scores:
Pred. No.: 3,05e-87 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-780-669-173 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAAGCAATTTCTTCTGCTGGGCGCTCTGTCATCCGACAGTGGTGTGAGCC 99
QY 21 AlaHisCysPheGlnAsnSerTrpThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCAGAACTCTACACCATCGGCTGGGCTGCAACAGCTTGAAGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTrpAsn 60
DB 160 CAAGACCCAGGAGCCAGATGTTGAGAGCCAGCTCTCCGTACAGGACCCAGAGTCAAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTCTGCTCTCAACGACCTCATGCTCATCAAGTTGACCAATCCGTCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACATCCGAGGACCATGCTTCCAGATGCCCTTACCCGGGGAACCTTTCCTC 339
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGCTGGGGGTCTGCTGGGGAACGAGTCAAGGTCGTGCTGCTCTTCA 399
QY 121 ArgArgSerSerIleGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGGAGGTCTCTCTCCGACCTGCGGGGCTGACCCAGAGCTCTGCTCCAGGAGAAATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTGTGACAGTGC 477

RESULT 5
US-09-030-606-173

Sequence 173, Application US/09030606
Patent No. US20020081580A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,606
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 1265 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-606-173

Alignment Scores:

Pred. No.:	3,05e-87	Length:	1265
Score:	758.00	Matches:	146
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-726-093-10 (1-146) x US-09-030-606-173 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValIleuValHisProGlnTrpValIleuSerAla 20
DB 40 ATGGAAACGAATGTTCTGCTCGGGCGTCTGGTGCAATCCGAGGGGTGCTGACGCC 99
QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTCCAGAACTCTACACCACTCGGCTGGCTGACAGCTCTTGAAGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60
DB 160 CAAGAGCCAGGAGCCAGATGGTGAGGCCAGCCTCTCGTAGCGCACCAGAGTACAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80
DB 220 AACACCTTCTCGCTAACACCACTCATCAAGTTGAGCAATCCGTTGTCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCAATCCGAGACATCAGACTTGTCCGACTGCTTACCCGGGGAAGCTTGGCTC 339
QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGGCTGGGCTGCTGCTGGGGAACGGTGAAGCTCAGCGGTGTGTGCTGCTCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGAGAGTCTCTGCTCCAGTGCAGGGGAGTGAACCAAGAGCTGTGCTCCAGGACAGATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTGTCTGCAAGTGGC 477

RESULT 6
US-09-822-827-173
; Sequence 173, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 173
; LENGTH: 1265
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1265)
; OTHER INFORMATION: n = A,T,C or G
US-09-822-827-173

Alignment Scores:

Pred. No.:	3,05e-87	Length:	1265
Score:	758.00	Matches:	146
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-726-093-10 (1-146) x US-09-822-827-173 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValIleuValHisProGlnTrpValIleuSerAla 20
DB 40 ATGGAAACGAATGTTCTGCTCGGGCGTCTGGTGCAATCCGAGGGGTGCTGACGCC 99
QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTCCAGAACTCTACACCACTCGGCTGGCTGACAGCTCTTGAAGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60
DB 160 CAAGAGCCAGGAGCCAGATGGTGAGGCCAGCCTCTCGTAGCGCACCAGAGTACAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80
DB 220 AACACCTTCTCGCTAACACCACTCATCAAGTTGAGCAATCCGTTGTCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCAATCCGAGACATCAGACTTGTCCGACTGCTTACCCGGGGAAGCTTGGCTC 339
QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGGCTGGGCTGCTGCTGGGGAACGGTGAAGCTCAGCGGTGTGTGCTGCTCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGAGAGTCTCTGCTCCAGTGCAGGGGAGTGAACCAAGAGCTGTGCTCCAGGACAGATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTGTCTGCAAGTGGC 477

RESULT 7
US-09-115-453-173
; Sequence 173, Application US/09115453B
; Patent No. US20020090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND

TITLE OF INVENTION: METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C4
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 173
LENGTH: 1265
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1265)
OTHER INFORMATION: n = A,T,C or G
US-09-115-453-173

Alignment Scores:
Pred. No.: 3,05e-87 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-726-093-10 (1-146) x US-09-115-453-173 (1-1265)

QY 1 MetGluAenGluLeuPheCySeSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAAGCAATTGTTCTGCTGGAGCTCTGTCATCCGACAGGGTGTCTGCAGCC 99
QY 21 AlaHisCySPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaasp 40
DB 100 GCACACTGTTCCAGAACTCTTACACCATCGGGCTGGCGCTGACAGTCTTGAGGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTrpAsn 60
DB 160 CAAGAGCCAGGAGCCAGATGTGTGAGGCGAGCTCTCGTACGACCCAGATACAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80
DB 220 AACCCCTGCTGCTTACGACCTCATGCTCATCAATGGACGAATCCGTCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCySProThrAlaGlyAsnSerCySleu 100
DB 280 GACACCATCCGAGATCAGCATTCCTTGCAGTCCCTACCGCGGGAATCTTCCCTC 339
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCySleuProSerSer 120
DB 340 GTTCTGGCTGGGCTGCTGCTGGGGAACGTGAGCTCACGGGTGTGTCTGCCCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCyS 140
DB 400 AGGAGGCTCTCTCCCGAGTGGGGGCTGACCCAGAGCTCTCGTCCGAGGAGATGC 459
QY 141 LeuProCySeSerAla 146
DB 460 CTACCGTCTGCAAGTCCG 477

RESULT 8
US-09-232-880-173
Sequence 173, Application US/09232880
Publication No. US20020182596A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.428C6
CURRENT APPLICATION NUMBER: US/09/232,880
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 173
LENGTH: 1265
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1265)
OTHER INFORMATION: n = A,T,C or G
US-09-232-880-173

Alignment Scores:
Pred. No.: 3,05e-87 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-726-093-10 (1-146) x US-09-232-880-173 (1-1265)

QY 1 MetGluAenGluLeuPheCySeSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAAGCAATTGTTCTGCTGGAGCTCTGTCATCCGACAGGGTGTCTGCAGCC 99
QY 21 AlaHisCySPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaasp 40
DB 100 GCACACTGTTCCAGAACTCTTACACCATCGGGCTGGCGCTGACAGTCTTGAGGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTrpAsn 60
DB 160 CAAGAGCCAGGAGCCAGATGTGTGAGGCGAGCTCTCGTACGACCCAGATACAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80
DB 220 AACCCCTGCTGCTTACGACCTCATGCTCATCAATGGACGAATCCGTCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCySProThrAlaGlyAsnSerCySleu 100
DB 280 GACACCATCCGAGATCAGCATTCCTTGCAGTCCCTACCGCGGGAATCTTCCCTC 339
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCySleuProSerSer 120
DB 340 GTTCTGGCTGGGCTGCTGCTGGGGAACGTGAGCTCACGGGTGTGTCTGCCCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCyS 140
DB 400 AGGAGGCTCTCTCCCGAGTGGGGGCTGACCCAGAGCTCTCGTCCGAGGAGATGC 459
QY 141 LeuProCySeSerAla 146
DB 460 CTACCGTCTGCAAGTCCG 477

RESULT 9
US-09-895-793-173
Sequence 173, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.

```

APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 173
LENGTH: 1265
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1265)
OTHER INFORMATION: n = A,T,C or G
US-09-895-793-173

```

```

Alignment Scores:
Pred. No.: 3.05e-87 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

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US-10-726-093-10 (1-146) x US-09-895-793-173 (1-1265)

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Qy 1 MetGluAnGluLeuPheCySeSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
Db 40 ATGAAAACGAATTGTTCTGCTCGGGGCTCTGTGTCATCCGACATGGGTCTGTCAACC 99
Qy 21 AlaHisCySpheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
Db 100 GCACACTGTTTCCAGAACTCTTACACCATCGGGCTGGCGACAGCTTGAGGCGGAC 159
Qy 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60
Db 160 CAAAGCCGAGGAGCCAGATGTGAGGCGACGCTCTCGTGAACGACCCAGAGTACAC 219
Qy 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
Db 220 AGACCTTGCTGCTTACGACCTCATGCTCATCAAGTTGGAGCAATCCGTCTCGAGTCT 279
Qy 81 AspThrIleArgSerIleSerIleAlaSerGlnCySpProThrAlaGlyAsnSerCysLeu 100
Db 280 GACACCATCCGAGATCAGCATTCCTCGCAGTGCCTTACCGCGGGAACCTTGCTTC 339
Qy 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
Db 340 GTTCTGCTGCTGGGTCTGCTGCGCAACGTAAGTCAAGGAGTGTGTCTCCCTCTTCA 399
Qy 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
Db 400 AGGAGGTCTCTGCGCACTCCGCGGGGCTGAACCCAGACTCTGCGGTCCCAAGCAATGC 459
Qy 141 LeuProCyCySerAla 146
Db 460 CTACCGTGTGCTGAGTGC 477

```

RESULT 10

```

US-09-895-814-173
Sequence 173, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.

```

```

APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 173
LENGTH: 1265
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1265)
OTHER INFORMATION: n = A,T,C or G
US-09-895-814-173

```

```

Alignment Scores:
Pred. No.: 3.05e-87 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

```

US-10-726-093-10 (1-146) x US-09-895-814-173 (1-1265)

```

Qy 1 MetGluAnGluLeuPheCySeSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
Db 40 ATGAAAACGAATTGTTCTGCTCGGGGCTCTGTGTCATCCGACATGGGTCTGTCAACC 99
Qy 21 AlaHisCySpheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
Db 100 GCACACTGTTTCCAGAACTCTTACACCATCGGGCTGGCGACAGCTTGAGGCGGAC 159
Qy 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60
Db 160 CAAAGCCGAGGAGCCAGATGTGAGGCGACGCTCTCGTGAACGACCCAGAGTACAC 219
Qy 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
Db 220 AGACCTTGCTGCTTACGACCTCATGCTCATCAAGTTGGAGCAATCCGTCTCGAGTCT 279
Qy 81 AspThrIleArgSerIleSerIleAlaSerGlnCySpProThrAlaGlyAsnSerCysLeu 100
Db 280 GACACCATCCGAGATCAGCATTCCTCGCAGTGCCTTACCGCGGGAACCTTGCTTC 339
Qy 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
Db 340 GTTCTGCTGCTGGGTCTGCTGCGCAACGTAAGTCAAGGAGTGTGTCTCCCTCTTCA 399
Qy 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
Db 400 AGGAGGTCTCTGCGCACTCCGCGGGGCTGAACCCAGACTCTGCGGTCCCAAGCAATGC 459

```

OY 141 LeuProCySeSerAla 146
DB 460 CTACCGTGTGCGAGTGGC 477

RESULT 11

US-10-012-896-173
Sequence 173, Application US/10012896

Publication No. US20020183251A1
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012.896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ. ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 173
LENGTH: 1265
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 967, 1094, 1095, 1115, 1126, 1154, 1174, 1176, 1212, 1251,
LOCATION: 1253
OTHER INFORMATION: n = A,T,C or G
US-10-012-896-173

Alignment Scores:

Pred. No.: 3.05e-87 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-726-093-10 (1-146) x US-10-012-896-173 (1-1265)

OY 1 MetGluAnGluLeuPheCySeSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAGAAAGCAATTGTTCTGCTCGGGGCTCTGTGGATCGCAGTGGGTCTGTGAGCC 99
OY 21 AlaHisCySePheGlnAenSerTyTrtTlleglyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACTCTTACACCATCGGGCTGGCCGCAAGTCTTGAGGCCGAC 159
OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyTrasn 60
DB 160 CAAAGCCAGGAGCCAGCATGTGAGGCCAGCTCTCCGTACGGACCCAGATGACAC 219

OY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AGACCCCTGTGCTGTACACCTCATGCTCATAGATGGAAGCAATCCGTTCGAGTCT 279
OY 81 AspThrIleArgSerIleSerIleAlaSerGlnCySeProThrAlaGlyAsnSerCyLeu 100
DB 280 GACACCATCCGAGCATCATGCTTGTGCGAGTGGCCATCCGGGGGAACTTGTCCCTC 339
OY 101 ValSerGlyTyPglyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGCTGGGGTCTGCTGCGGAAAGGTGAGCTCACCGGAGTGTGTCTGCTTGA 399
OY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlyCy 140
DB 400 AGAGAGTCTGTGCGCCAGTGGCGGGGCTGACCCAGAGCTTGTGCTCCAGCAGAAATGC 459
OY 141 LeuProCySeSerAla 146
DB 460 CTACCGTGTGCGAGTGGC 477

RESULT 12

US-10-010-940-173
Sequence 173, Application US/10010940

Publication No. US20030088062A1
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427D3
CURRENT APPLICATION NUMBER: US/10/010.940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ. ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 173
LENGTH: 1265
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1265)
OTHER INFORMATION: n = A,T,C or G
US-10-010-940-173

Alignment Scores:

Pred. No.: 3.05e-87 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-726-093-10 (1-146) x US-10-010-940-173 (1-1265)

OY 1 MetGluAnGluLeuPheCySeSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAGAAAGCAATTGTTCTGCTCGGGGCTCTGTGGATCGCAGTGGGTCTGTGAGCC 99
OY 21 AlaHisCySePheGlnAenSerTyTrtTlleglyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACTCTTACACCATCGGGCTGGCCGCAAGTCTTGAGGCCGAC 159
OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyTrasn 60


```

DB      160 CAAGAGCCGAGGAGCCAGATGGAGGAGCCAGCTCTCGTACGAGCAGCCAGACAGTACAAAC 219
QY      61 AAGPProleuleuAlaAsnAspLeuMetLeuIleYsLeuAspGluSerValSerGluSer 80
DB      220 AARCCCTTCTGCTGCTACACACTGCTCATCTCACTTGGAGAAATCCGTGCTCCAGTCTT 279
QY      81 AsPThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB      280 GACACATCCGAGAGCATCAGATTGCTTCGAGTGCCCTACCGGGGAACTCTTGCCCTC 339
QY      101 ValSerGlyThrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB      340 GTTCTGGCTGGGGTCTGCTGCGAAGCGGTGAGCTCAGCGGGTGTGTCTGCTCTTCA 399
QY      121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB      400 AGGAGGCTCTTCTGCTCCAGTCCGCGGGGCTGACCCAGAGCTTCTGCTCCAGGAGAAATCC 459
QY      141 LeuProCysCysSerAla 146
DB      460 CTACCGTCTGCTGAGTGGC 477

RESULT 13
US-10-144-678A-173
; Sequence 173, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Basols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 173
; LENGTH: 1265
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 967, 1094, 1095, 1115, 1126, 1154, 1174, 1212, 1251,
; LOCATION: 1253
; OTHER INFORMATION: n = A,T,C or G
US-10-144-678A-173

Alignment Scores:
Pred. No.: 3,05e-87 Length: 1265
Score: 758.00 Matches: 146
Best Local Similarity: 100.0%
Percent Similarity: 100.0%
Query Match: 7 Gaps: 0
DB: 7

```

```

Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-726-093-10 (1-146) x US-10-144-678A-173 (1-1265)

QY      1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB      40 ATGAAAAAGCAATGTCTTCTGCGGCGTCTGTGATCCGACATGGGTCTGTCAACC 99
QY      21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB      100 GCACACTGTTTCCAGAACTCTTACACATCGGGCTGGGCTGGCCAGACTTGAGGCCGAC 159
QY      41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60
DB      160 CAAGAGCCAGGAGCAGATGATGTGAGGCCAGCTCTCCGTAACGAGCAGACCCAGATACAAAC 219
QY      61 ArgProleuleuAlaAsnAspLeuMetLeuIleYsLeuAspGluSerValSerGluSer 80
DB      220 AGACCTTCTGCTGCTTACAGACTCATGCTCATGAGTGAAGAGCAATCGTGTCCAGTCT 279
QY      81 AsPThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB      280 GACACATCCGAGAGCATCAGATTGCTTCGAGTGCCCTACCGGGGAACTCTTGCCCTC 339
QY      101 ValSerGlyThrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB      340 GTTCTGGCTGGGGTCTGCTGCGAAGCGGTGAGCTCAGCGGGTGTGTCTGCTCTTCA 399
QY      121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB      400 AGGAGGCTCTTCTGCTCCAGTCCGCGGGGCTGACCCAGAGCTTCTGCTCCAGGAGAAATCC 459
QY      141 LeuProCysCysSerAla 146
DB      460 CTACCGTCTGCTGAGTGGC 477

RESULT 14
US-10-294-025-173
; Sequence 173, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 173
; LENGTH: 1265
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 967, 1094, 1095, 1115, 1126, 1154, 1174, 1176, 1212, 1251,
; LOCATION: 1253
; OTHER INFORMATION: n = A,T,C or G
US-10-294-025-173

Alignment Scores:
Pred. No.: 3,05e-87 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

```

US-10-726-093-10 (1-146) x US-10-294-025-173 (1-1265)

OY 1 MetGluAenGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
 DB 40 ATGGAAACGAAATTTCTTCTCGGCGCTCTGTCGATCCGCACTGGGTGTCACGCC 99
 OY 21 AlaHisCysPheGlnAenSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
 DB 100 GCACACTGTTTCCAGAACTCTTACACCATCGGGCTGGGCTGCACAGTCTTGAGGCCGAC 159
 OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyTrsn 60
 DB 160 CAAGAGCCAGGAGCCAGATGTGTGAGGCGACCTCTCCGTACGGACCCAGAGTACAAAC 219
 OY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
 DB 220 AGACCTTGCTGCTGCTAACGACTCATGCTCATCAAGTTGAGCAAGATCCGTGCCAGTCT 279
 OY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
 DB 280 GACACCATCCGAGCATTCAGCATTCCTGCTGCGAGTCCCTTACCCGGGGAACTTTGCCCTC 339
 OY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
 DB 340 GTTCTGGCTGGGGTGTGCTGTGGGAACTGAGCTCAGGGGTGTGTCTGCCCTTTCA 399
 OY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
 DB 400 AGAGAGTCTCTGCGCCAGTCCGCGGGGCTGACCCAGAGCTTGTCCCTCCAGGAGAAATGC 459
 OY 141 LeuProCysCysSerAla 146
 DB 460 CTACCGTCTGCAGTCCG 477

RESULT 15

US-10-688-838-173

Sequence 173, Application US/10688838

Publication No. US20040141989A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

FILE REFERENCE: 210121.427D4

CURRENT APPLICATION NUMBER: US/10/688,838

NUMBER OF SEQ ID NOS: 228

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 173

LENGTH: 1265

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: 967, 1094, 1095, 1115, 1126, 1154, 1174, 1176, 1212, 1251,

LOCATION: 1253

OTHER INFORMATION: n = A,T,C or G

US-10-688-838-173

Alignment Scores:

Pred. No.: 3,05e-87

Score: 758.00

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Query Match: 100.0%

DB: 8

US-10-726-093-10 (1-146) x US-10-688-838-173 (1-1265)

OY 21 AlaHisCysPheGlnAenSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
 DB 100 GCACACTGTTTCCAGAACTCTTACACCATCGGGCTGGGCTGCACAGTCTTGAGGCCGAC 159
 OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyTrsn 60
 DB 160 CAAGAGCCAGGAGCCAGATGTGTGAGGCGACCTCTCCGTACGGACCCAGAGTACAAAC 219
 OY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
 DB 220 AGACCTTGCTGCTGCTAACGACTCATGCTCATCAAGTTGAGCAAGATCCGTGCCAGTCT 279
 OY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
 DB 280 GACACCATCCGAGCATTCAGCATTCCTGCTGCGAGTCCCTTACCCGGGGAACTTTGCCCTC 339
 OY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
 DB 340 GTTCTGGCTGGGGTGTGCTGTGGGAACTGAGCTCAGGGGTGTGTCTGCCCTTTCA 399
 OY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
 DB 400 AGAGAGTCTCTGCGCCAGTCCGCGGGGCTGACCCAGAGCTTGTCCCTCCAGGAGAAATGC 459
 OY 141 LeuProCysCysSerAla 146
 DB 460 CTACCGTCTGCAGTCCG 477

Search completed: August 28, 2006, 18:46:07
 Job time : 1075 secs

OY 1 MetGluAenGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
 DB 40 ATGGAAACGAAATTTCTTCTCGGCGCTCTGTCGATCCGCACTGGGTGTCACGCC 99

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OW protein - protein search, using sw model

Run on: August 29, 2006, 03:38:09 ; Search time 196 Seconds
(without alignments)
340.580 Million cell updates/sec

Title: US-10-726-093-10

Perfect score: 758
Sequence: 1 MENELFCGVLVHPQWLSA.....SRGLTQSSASQAELPCCSA 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: A_Geneseq_8:
2: geneseqp1980s:
3: geneseqp1990s:
4: geneseqp2000s:
5: geneseqp2001s:
6: geneseqp2002s:
7: geneseqp2003s:
8: geneseqp2004s:
9: geneseqp2005s:
10: geneseqp2006s:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	758	100.0	146	AAB50449	Aab50449 Human pro
2	758	100.0	195	ABP54355	ABP54355 Human KTK
3	594	78.4	237	AAB21293	Aab21293 Human KTK
4	577	76.1	164	AAW69389	Aaw69389 Prostate
5	577	76.1	164	AAW71873	Aaw71873 Protein e
6	577	76.1	164	AAW82006	Aay82006 Human imm
7	577	76.1	164	ABG94415	Abg94415 Human pro
8	577	76.1	164	AAW01121	Aam01121 Human pro
9	577	76.1	164	AAU69767	Aau69767 Human pro
10	577	76.1	164	AAW74804	Aab74804 Prostate
11	577	76.1	164	AAW74804	Aab74804 Prostate
12	577	76.1	164	ABU71657	Abu71657 Prostate
13	577	76.1	164	AAU04965	Aau04965 Human pro
14	577	76.1	164	ABP54355	ABP54355 Human pro
15	577	76.1	164	ABP54355	ABP54355 Human pro
16	577	76.1	164	ABP54355	ABP54355 Human pro
17	577	76.1	164	ABP54355	ABP54355 Human pro
18	577	76.1	164	ABP54355	ABP54355 Human pro
19	577	76.1	164	ABP54355	ABP54355 Human pro
20	577	76.1	205	AAW82006	Aay82006 Human pro
21	577	76.1	220	AAW82008	Aay82008 Human imm
22	577	76.1	220	AAW82008	Aay82008 Human imm
23	577	76.1	220	AAW82008	Aay82008 Human pro

24	577	76.1	220	4	AAB74806	Aab74806 Prostate
25	577	76.1	220	4	AAW99008	Aaw99008 Human pro
26	577	76.1	220	4	AAW62147	Aag62147 Human pro
27	577	76.1	220	4	ABU71659	Abu71659 Prostate
28	577	76.1	220	5	ABP54340	Abp54340 Human pro
29	577	76.1	220	6	ABP54340	Abp54340 Prostate
30	577	76.1	220	7	ADG26193	Adg26193 Human pro
31	577	76.1	220	7	AEF66474	Aef66474 Human pro
32	577	76.1	220	10	AEF66474	Aef66474 Human pro
33	577	76.1	226	4	AAW72526	Aay72526 Human pro
34	577	76.1	226	5	AAU74902	Aau74902 Protein s
35	577	76.1	226	5	AAU74933	Aau74933 Amino aci
36	577	76.1	231	2	AAW25510	Aay25510 Human pro
37	577	76.1	231	2	AAE00397	Aae00397 Human ser
38	577	76.1	249	3	AAW21307	Aab21307 Human pro
39	577	76.1	253	3	AAW21308	Aab21308 Human EMS
40	577	76.1	254	3	AAW21320	Aab21320 Human pro
41	577	76.1	254	3	AAW21294	Aab21294 Human KTK
42	577	76.1	254	3	AAW72525	Aay72525 Human pro
43	577	76.1	254	4	AAW01174	Aam01174 Human pro
44	577	76.1	254	4	AAU69819	Aau69819 Human pro
45	577	76.1	254	4	AAW99059	Aag99059 Human pro

ALIGNMENTS

RESULT 1	AAB50449	AAB50449 standard; protein; 146 AA.
ID	AAB50449	
XX	XX	
AC	AAW50449;	
DT	14-MAR-2001 (first entry)	
XX	XX	
DE	Human prostate cancer-related intracellular protein #3.	
XX	XX	
KW	Human; prostate cancer; intracellular protein; cytosolic; gene therapy; breast cancer.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
PN	MO200071711-A2.	
XX	XX	
PD	30-NOV-2000.	
XX	XX	
PF	19-MAY-2000; 2000MO-IB000673.	
XX	XX	
PR	20-MAY-1999; 99US-0135325P.	
XX	XX	
PR	20-MAY-1999; 99US-0135333P.	
XX	XX	
PA	(SAAT/) SAATCIOGLU F.	
XX	XX	
PI	Saatcioglu F;	
XX	XX	
DR	WPI, 2001-032036/04.	
XX	XX	
DR	N-PSDB; AAC90119, AAC90126.	
XX	XX	
PT	Novel nucleic acids encoding intracellular proteins useful for detecting neoplastic cell in a mammal, preferably the presence of prostate cancer or breast cancer.	
XX	XX	
PS	Claim 27; Page 23-24; 47pp; English.	
XX	XX	
CC	The present sequence is an intracellular protein which is encoded by a gene that is differentially expressed in neoplastic cells, particularly prostate cancer cells. The polynucleotides and polypeptides are useful for diagnosing or detecting prostate cancer and breast cancer cells. The polynucleotides and polypeptides are also useful for treating cancer by antisense therapy, and antibody based therapy, respectively. Note; The present sequence is given as SEQ ID NO: 17 in the sequence listing. SEQ ID NO: 17 is referred to in claim 27, but is described as an RNA molecule, rather than as a polypeptide	

XX Sequence 146 AA;
SQ
Query Match 100.0%; Score 758; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.7e-63;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MENELFCGVLVHPQWLSAAHCFONSYYTIGLHSLLEADQEPGSOVWEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWLSAAHCFONSYYTIGLHSLLEADQEPGSOVWEASLSVRHPEYN 60
OY 61 RPLLANDMLIKLDESVSSEDTRISISIASOCPAGNSCLVSGWGLANGELTGVCPLSS 120
DB 61 RPLLANDMLIKLDESVSSEDTRISISIASOCPAGNSCLVSGWGLANGELTGVCPLSS 120
OY 121 RRSSAOSRGLTOSASQAECPLCCSA 146
DB 121 RRSSAOSRGLTOSASQAECPLCCSA 146
RESULT 2
ID AABP54355 standard; protein; 195 AA.
XX AABP54355;
AC AABP54355;
DT 20-JAN-2003 (first entry)
XX
DE Human KLK4 alternatively spliced variant protein SEQ ID NO:2.
XX
KW Human; KLK4; cancer; benign tumour; cytostatic; variant.
XX
OS Homo sapiens.
XX
PN WO200277243-A1.
XX
PD 03-OCT-2002.
XX
PF 27-MAR-2002; 2002WO-AU000378.
XX
PR 27-MAR-2001; 2001AU-00004022.
XX
PA (UYOU-) UNIV QUEENSLAND TECHNOLOGY.
XX
PI Dong Y, Clements JA;
XX
DR MPI: 2003-029939/02.
XX
N-PSDB; ABQ83341.
XX
PT Detecting the presence or diagnosing the risk of cancer or benign tumor,
PT e.g. an ovarian, endometrial or prostate cancer, by determining the
PT presence of or detecting aberrant expression of KLK4 in a biological
PT sample from the patient.
XX
PS Claim 83; Fig 7; 126pp; English.
XX
XX The present invention describes a method (M1) for detecting the presence
XX or diagnosing the risk of cancer or benign tumour in a patient. M1
XX comprises determining the presence of or detecting aberrant expression of
XX KLK4 in a biological sample obtained from the patient. KLK4 has
XX cytostatic activity. The method is useful for detecting the presence or
XX diagnosing the risk of a cancer or a benign tumour in a patient,
XX particularly an ovarian, endometrial or prostate cancer, or a cancer or
XX benign tumour associated with an organ or tissue from the ovaries,
XX endometrium or prostate. An agent which can be used for restoring or
XX modulating KLK4 expression can be used for treating or preventing cancer
XX or benign tumour. KLK4 polynucleotides, polypeptides or antigen-binding
XX molecules from the present invention can be used for detecting aberrant
XX KLK4 polynucleotides or aberrant K4 polypeptides that correlate with a
XX cancer or a benign tumour. The present sequence represents a human KLK4
XX alternatively spliced variant from the present invention
SQ Sequence 195 AA;

Query Match 100.0%; Score 758; DB 6; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.4e-63;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MENELFCGVLVHPQWLSAAHCFONSYYTIGLHSLLEADQEPGSOVWEASLSVRHPEYN 60
DB 50 MENELFCGVLVHPQWLSAAHCFONSYYTIGLHSLLEADQEPGSOVWEASLSVRHPEYN 109
OY 61 RPLLANDMLIKLDESVSSEDTRISISIASOCPAGNSCLVSGWGLANGELTGVCPLSS 120
DB 110 RPLLANDMLIKLDESVSSEDTRISISIASOCPAGNSCLVSGWGLANGELTGVCPLSS 169
OY 121 RRSSAOSRGLTOSASQAECPLCCSA 146
DB 170 RRSSAOSRGLTOSASQAECPLCCSA 195
RESULT 3
ID AAB21293 standard; protein; 237 AA.
XX AAB21293;
AC AAB21293;
DT 02-FEB-2001 (first entry)
XX
DE Human KLK-L1 protein #1.
XX
KW Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6;
KW kallikrein-like protein; serine protease; cytostatic; cancer;
KW prostate cancer.
XX
OS Homo sapiens.
XX
PN WO200053776-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-CA000258.
XX
PR 11-MAR-1999; 99US-0124260P.
PR 01-APR-1999; 99US-0127386P.
PR 21-JUL-1999; 99US-0144919P.
XX
PA (MOUN) MOUNT SINAI HOSPITAL.
XX
PI Yousef GM, Diamandis EP;
XX
DR MPI: 2000-587440/55.
XX
N-PSDB; AAA95896.
XX
PT New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L
PT protein mediated disorders, especially cancer.
XX
PS Claim 8; Page 141; 184pp; English.
XX
XX The present sequence is kallikrein-like protein KLK-L1. Kallikreins and
XX kallikrein-like proteins are a subgroup of the serine protease enzyme
XX family. They catalyze the selective cleavage of specific polypeptide
XX precursors to release peptides with potent biological activity. Nucleic
XX acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4,
XX KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the
XX treatment, monitoring and diagnosis of cancers, especially prostate
XX cancer. They can also be used to identify a substance that can associate
XX with or mediate the biological activity of the proteins. Antibodies can
XX be used to treat conditions mediated by the kallikrein-like proteins
SQ Sequence 237 AA;
Query Match 78.4%; Score 594; DB 3; Length 237;
Best Local Similarity 100.0%; Pred. No. 9.2e-48;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MENELFCGVLVHPQWVLSAHCFOFNSYTTIGLHSLLEADQEPGSOVWEASLSVRHPEYN 60
 DB 29 MENELFCGVLVHPQWVLSAHCFOFNSYTTIGLHSLLEADQEPGSOVWEASLSVRHPEYN 88
 OY 61 RPLANDMLIKLDESSESPTIRISISASOCPPTAGNSCLVSGWGLANGELTG 114
 DB 89 RPLANDMLIKLDESSESPTIRISISASOCPPTAGNSCLVSGWGLANGELTG 142

RESULT 4

ID AAW69389 standard; protein; 164 AA.

AAW69389;

25-MAR-2003 (revised)
 08-DEC-1998 (first entry)

Prostate tumour specific gene clone DE14 protein.

Prostate tumour specific gene; human; prostate cancer; detection;

therapy.

Homo sapiens.

Key Location/Qualifiers

Misc-difference 118 /note= "unspecified amino acid"

MO9837418-A2.

27-AUG-1998.

25-FEB-1998; 98WO-US003690.

25-FEB-1997; 97US-00806596.

01-AUG-1997; 97US-00904809.

09-FEB-1998; 98US-00020747.

(CORI-) CORIXA CORP.

Xu J, Dillon DC;

WPI; 1998-480805/41.

N-PSDB; AAV58648.

Novel human prostate specific tumour protein and fragments - useful for

detecting and treating prostate cancers.

Example 1; Page 117-118; 141pp; English.

This sequence is encoded by a human prostate tumour specific gene, and

can be used in the method of the invention. The method is for detecting

prostate cancer comprising contacting a biological sample with an agent

able to bind an immunogenic portion of a prostate protein (such as this

protein sequence). An antibody which binds to an immunogenic portion of

the prostate protein, and the method can be used to detect, monitor

progression of, or treat prostate cancers. The antibody may also be

conjugated to a therapeutic agent for use in therapy of prostate cancers.

(updated on 25-MAR-2003 to correct PR field.)

Sequence 164 AA:

Query Match 76.1%; Score 577; DB 2; Length 164;

Best Local Similarity 77.1%; Pred. No. 2.4e-46; Indels 14; Gaps 3;

Matches 118; Conservative 5; Mismatches 16;

1 MENELFCGVLVHPQWVLSAHCFOFNSYTTIGLHSLLEADQEPGSOVWEASLSVRHPEYN 60

1 MENELFCGVLVHPQWVLSAHCFOFNSYTTIGLHSLLEADQEPGSOVWEASLSVRHPEYN 60

61 RPLANDMLIKLDESSESPTIRISISASOCPPTAGNSCLVSGWGLANGELTG----- 115

DB 61 RPLANDMLIKLDESSESPTIRISISASOCPPTAGNSCLVSGWGLANDAVIAIOSXTV 120

OY 116 -----CLPSSRRSSAQSRLTQSSASQAECCLPCC 144

DB 121 GWEC-----EKLSPWOGCTISATSSAR-TSCC 148

RESULT 5

AAW71873 standard; protein; 164 AA.

AAW71873;

06-JAN-1999 (first entry)

Protein encoded by prostate tumour clone P703 splice variant DE14.

Prostate; cancer; tumour; vaccine; immunogen; clone.

Homo sapiens.

Key Location/Qualifiers

Misc-difference 118 /note= "undefined residue"

MO9837093-A2.

27-AUG-1998.

25-FEB-1998; 98WO-US003492.

25-FEB-1997; 97US-00806099.

01-AUG-1997; 97US-00904804.

09-FEB-1998; 98US-00020956.

(CORI-) CORIXA CORP.

Xu J, Dillon DC;

WPI; 1998-609886/51.

Polypeptides comprising immunogenic portions of prostate proteins - used

in a vaccine for the treatment of prostate cancer.

Example 3; Page 109; 130pp; English.

The present sequence is an immunogenic portion of a prostate tumour

protein. The immunogen, or the DNA encoding it, can be used as a vaccine

for the treatment of prostate cancer. The immunogen was isolated from a

prostate tumour cDNA library obtained by subcloning a prostate tumour

cDNA expression library with a normal tissue cDNA library

Sequence 164 AA:

Query Match 76.1%; Score 577; DB 2; Length 164;

Best Local Similarity 77.1%; Pred. No. 2.4e-46; Indels 14; Gaps 3;

Matches 118; Conservative 5; Mismatches 16;

1 MENELFCGVLVHPQWVLSAHCFOFNSYTTIGLHSLLEADQEPGSOVWEASLSVRHPEYN 60

1 MENELFCGVLVHPQWVLSAHCFOFNSYTTIGLHSLLEADQEPGSOVWEASLSVRHPEYN 60

61 RPLANDMLIKLDESSESPTIRISISASOCPPTAGNSCLVSGWGLANGELTG----- 115

61 RPLANDMLIKLDESSESPTIRISISASOCPPTAGNSCLVSGWGLANDAVIAIOSXTV 120

116 -----CLPSSRRSSAQSRLTQSSASQAECCLPCC 144

121 GWEC-----EKLSPWOGCTISATSSAR-TSCC 148

RESULT 6
 AAY82006

```
ID AAY82006 standard; protein; 164 AA.
XX
XX AAY82006;
AC
XX
XX 13-JUN-2000 (first entry)
DT
XX
XX Human immunogenic prostate tumour protein sequence SEQ ID NO:178.
DE
XX
XX Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
XX immunogenic; cytostatic; vaccine.
XX
XX Homo sapiens.
OS
XX WO200004149-A2.
PN
XX
XX 27-JAN-2000.
PD
XX
XX 14-JUL-1999; 99WO-US015838.
PP
XX
XX 14-JUL-1998; 98US-00115453.
PR
XX 14-JUL-1998; 98US-00116134.
PR 23-SEP-1998; 98US-00159812.
PR 23-SEP-1998; 98US-00159822.
PR 15-JAN-1999; 98US-00232149.
PR 15-JAN-1999; 99US-00232880.
PR 09-APR-1999; 99US-00288946.
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX
XX WPI; 2000-171268/15.
DR
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein.
XX
XX Claim 3; Page 160; 263pp; English.
XX
XX The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express the
CC polypeptides, antibodies against the polypeptides and vaccines comprising
CC them can be used for inhibiting the development of prostate cancer in a
CC patient. The polypeptides can be used to generate antibodies or anti-
CC idiotypic antibodies for passive immuno therapy. A portion of the
CC polynucleotides encoding the polypeptides can be used as a probe or to
CC modulate the expression of the polypeptides. AA06241 to AA06691 and
CC AAY82000 to AAY82020 represent sequences used in the exemplification of
CC the present invention
XX
XX Sequence 164 AA;
SQ
Query Match 76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 2,4e-46;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;
OY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGSOVWEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGSOVWEASLSVRHPEYN 60
OY 61 RPLLANDMLIKLDESSESDDTIRISISIASQCPTAGNSCLVSGWGLANGELTGV----- 115
DB 61 RPLLANDMLIKLDESSESDDTIRISISIASQCPTAGNSCLVSGWGLANGELTGV----- 115
OY 116 -----CLPSSRRSSAQSRLTQSSASQAELPCC 144
DB 116 -----CLPSSRRSSAQSRLTQSSASQAELPCC 144
OY 121 GWMEC-----EKLSPWQGGCTISATSSAR-TSCC 148
DB 121 GWMEC-----EKLSPWQGGCTISATSSAR-TSCC 148
RESULT 7
ABG94415
```

```
ID ABG94415 standard; protein; 164 AA.
XX
XX ABG94415;
AC
XX
XX 27-NOV-2002 (first entry)
DT
XX
XX Human prostate tumour protein partial variant sequence #3.
DE
XX
XX Human; immunogenic; prostate protein; prostate tumour protein;
XX prostate cancer; cytostatic; vaccine.
XX
XX Homo sapiens.
OS
XX US2002090372-A1.
PN
XX
XX 11-JUL-2002.
PD
XX
XX 14-JUL-1998; 98US-00115453.
PP
XX
XX 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
XX
XX (XUJ/) XU J.
PA (DILL/) DILLON D C.
XX
XX Xu J, Dillon DC;
XX
XX WPI; 2000-171268/15.
DR N-PSDB; ABS71316.
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein.
XX
XX Example 3; Page 82; 101pp; English.
XX
XX The present invention relates to a new polypeptide comprising an
CC immunogenic portion of a prostate protein. The invention is useful for
CC inhibiting the development of prostate cancer in a patient. The invention
CC is also useful as markers for diagnosing prostate cancer and for
CC monitoring diseases progression in patients. The present amino acid
CC sequence represents a variant human prostate tumour protein
XX
XX Sequence 164 AA;
SQ
Query Match 76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 2,4e-46;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;
OY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGSOVWEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGSOVWEASLSVRHPEYN 60
OY 61 RPLLANDMLIKLDESSESDDTIRISISIASQCPTAGNSCLVSGWGLANGELTGV----- 115
DB 61 RPLLANDMLIKLDESSESDDTIRISISIASQCPTAGNSCLVSGWGLANGELTGV----- 115
OY 116 -----CLPSSRRSSAQSRLTQSSASQAELPCC 144
DB 116 -----CLPSSRRSSAQSRLTQSSASQAELPCC 144
OY 121 GWMEC-----EKLSPWQGGCTISATSSAR-TSCC 148
DB 121 GWMEC-----EKLSPWQGGCTISATSSAR-TSCC 148
RESULT 8
AA001121
ID AA001121 standard; protein; 164 AA.
XX
XX AA001121;
AC
XX
XX 04-OCT-2001 (first entry)
DT
XX
XX Human prostate-specific amino acid sequence P703P-DE14.
XX
```

XX	Human; prostate cancer; prostate-specific; diagnosis; vaccine;	
KM	cytostatic; gene therapy; metastasis.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200151633-A2.	
XX		
XX	19-JUL-2001.	
XX		
PF	16-JAN-2001; 2001WO-US001574.	
XX		
PI	14-JAN-2000; 2000US-00483672.	
XX		
PA	(CORI-) CORIXA CORP.	
XX		
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;	
PI	Kalos MD, Fanger GR, Day CH, Retter MM, Stolk JA, Skelky YAW;	
PI	Wang A, Meagher MJ;	
DR	WPI; 2001-425873/45.	
XX		
PT	New polynucleotide encoding a prostate-specific protein, for diagnosing,	
PT	monitoring and treating prostate cancer in a patient and for use in	
PT	vaccines.	
XX		
PS	Claim 2; Page 288; 543pp; English.	
XX		
CC	The present invention describes polynucleotide sequences (I) which encode	
CC	prostate-specific proteins (II). (I) and (II) have cytostatic activity,	
CC	and can be used in vaccine production and gene therapy. (I), (II),	
CC	antibodies to (II), fusion proteins comprising (II), and isolated T cells	
CC	prepared using (I) or (II) are used to treat cancer in a patient. (I) and	
CC	the antibodies are also used in the detection of cancer in a patient. The	
CC	cancer that is diagnosed or treated is particularly prostate cancer. (I)	
CC	and (II) can be used in vaccines. The antibodies or (I) can be used for	
CC	monitoring the progression of cancer in a patient. (I) and (II) can also	
CC	be used to improve diagnostic and therapeutic methods for prostate	
CC	cancer. They can indicate the level of metastasis as well as the prostate	
CC	volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent	
CC	polynucleotide and amino acid sequences used in the exemplification of	
CC	the present invention	
XX		
SQ	Sequence 164 AA;	
XX		
XX	Query Match	76.1%; Score 577; DB 4; Length 164;
XX	Best Local Similarity	77.1%; Pred. No. 2, 4e-46;
XX	Matches 118; Conservative	5; Mismatches 16; Indels 14; Gaps 3.
QY	1 MENELFCGSGVLVHPQWVLSAAHCFQNSYITIGLGLHSLELDDPFGSQMWVASLSVHHPEYN	60
DB	1 MENELFCGSGVLVHPQWVLSAAHCFQNSYITIGLGLHSLELDDPFGSQMWVASLSVHHPEYN	60
QY	61 RLPLNDMLIKLDESVSSEDTIRISIASOCPTAGNSCLTVSGWGLLANGEITGV-----	115
DB	61 RLPLNDMLIKLDESVSSEDTIRISIASOCPTAGNSCLTVSGWGLLANGEITGV-----	120
QY	116 ----CLPSSRRSSAQSRLGTQSSASQAQELPCC	144
DB	121 GGWEC----EKLSQPMQGCTIATTSAR-TSCC	148
XX		
XX	RESULT 9	
XX	AAU69767	
XX	ID AAU69767 standard; protein; 164 AA.	
XX	AAU69767;	
XX		
DT	30-JAN-2002 (first entry)	
XX		
DE	Human prostate cDNA encoded protein #7.	
XX		
XX	Human; prostate cancer; cytostatic; immunostimulant; tumour; immunogen.	
XX		

XX	Homo sapiens.
XX	
PN	WO200173032-A2.
PD	
XX	04-OCT-2001.
XX	
PF	27-MAR-2001; 200iWO-US009919.
XX	
PR	27-MAR-2000; 2000US-00536857.
PR	09-MAY-2000; 2000US-00568100.
PR	12-MAY-2000; 2000US-00570737.
PR	13-JUN-2000; 2000US-00593793.
PR	27-JUN-2000; 2000US-00605783.
PR	09-AUG-2000; 2000US-00636215.
PR	29-AUG-2000; 2000US-00651236.
PR	06-SEP-2000; 2000US-00657279.
PR	02-OCT-2000; 2000US-00679426.
PR	10-OCT-2000; 2000US-00685166.
PR	09-NOV-2000; 2000US-00709729.
XX	
PA	(CORI-) CORIXA CORP.
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI	Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI	Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;
XX	
DR	WPI; 2001-639232/73.
DR	N-PSDB; AAS63619.
XX	
PT	New human prostate-specific polypeptides and polynucleotides useful for
PT	the diagnosis and treatment of cancer, especially prostate cancer.
PS	
XX	Claim 2; Page 290; 579pp; English.
XX	
CC	The invention relates to isolated prostate-specific polynucleotides,
CC	polypeptides, fusion proteins of the polypeptides, antibodies raised
CC	against the polypeptides (or antigenic epitopes derived from them) and
CC	antigen-presenting cells expressing the polypeptides. The antibodies are
CC	useful for detecting the presence of cancer, especially prostate cancer.
CC	The polypeptides, polynucleotides and the antigen-presenting cells are
CC	useful for stimulating and/or expanding T cells specific for a tumour
CC	protein, and for inhibiting the development of cancer especially prostate
CC	cancer. Compositions comprising the polynucleotide and/or polypeptide are
CC	useful for stimulating an immune response, and for treating cancer. The
CC	oligonucleotide is useful for detecting cancer. The present sequence is a
CC	prostate specific polypeptide of the invention
XX	
XX	
SO	Sequence 164 AA;
	Query Match 76.1%; Score 577; DB 4; Length 164;
	Best Local Similarity 77.1%; Pred. No. 2.4e-46;
	Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3.
Qy	1 MENELFCGCVLHPQWVLSAACHFONSYYTIGLGLHSLLEADDPGSGMVEASLSVHPHYN 60
Db	1 MENELFCGCVLHPQWVLSAACHFONSYYTIGLGLHSLLEADDPGSGMVEASLSVHPHYN 60
Qy	61 RPLANDMLITLDSVSRSQTRISIASOCPFGNSCLVSGWGLANGLTGV----- 115
Db	61 RPLANDMLITLDSVSRSQTRISIASOCPFGNSCLVSGWGLANGLTGV----- 115
Qy	116 ----CLPSSRRSSAOSRGITQSSASQAECCLPCC 144
Db	121 GGMEC-----EXLSOPMGCTTATSSAR-TSCC 148
RESULT 10	
AAB74804	
ID	AAB74804 standard; protein; 164 AA.
XX	
AC	AAB74804;
XX	
DT	14-JUN-2001 (first entry)

XX Prostate tumour antigen predicted amino acid sequence for P703P-DE14.
DE Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
XX prostate cancer; immunogenic; cytostatic; vaccine.
XX Homo sapiens.
XX WO200125272-A2.
XX 12-APR-2001.
XX 04-OCT-2000; 2000WO-US027464.
XX 04-OCT-1999; 99US-0157455P.
XX (CORI-) CORIXA CORP.
XX Xu J, Skeiky YAM, Reed SG, Cheever MA,
XX WPI; 2001-245062/25.
XX N-PSDB; AAH02592.
XX Prostate specific protein and its encoding polynucleotide, useful for the
PT treatment and diagnosis of prostate cancer.
XX Claim 3; Page 177; 276pp; English.
XX The present invention describes an isolated polypeptide (I) comprising at
CC least an immunogenic portion of a prostate tumour antigen protein or its
CC variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I), prostate tumour antigen polynucleotides, an antigen
CC desending cell (APC e.g. a dendritic cell) that expresses (I), and a
CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a polynucleotide
CC that encodes a prostate specific protein are useful for detecting the
CC presence or absence of a cancer or monitoring the progression of the
CC progression of a cancer, especially prostate cancer. AAH02422 to AAH2872,
CC AAB74798 to AAB74821 and AAB74830 are sequences used in the
CC exemplification of the present invention
XX Sequence 164 AA;
SQ
Query Match 76.1%; Score 577; DB 4; Length 164;
Best Local Similarity 77.1%; Pred. No. 2,4e-46;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;
QY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGSGQWVEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGSGQWVEASLSVRHPEYN 60
QY 61 RPLLANDMLIKLDESVESDTRISISIASOCPAGNSCLVSGWGLANGELTGV----- 115
DB 61 RPLLANDMLIKLDESVESDTRISISIASOCPAGNSCLVSGWGLANGELTGV----- 115
QY 116 ----CLPSSRRSSAOSRGLTOSASQAECUPCC 144
DB 121 GMEWC-----EKLSPWOGCTISATSSAR-TSCC 148
RESULT 11
AAG99006 standard; protein; 164 AA.
XX AAG99006;
XX 25-SEP-2001 (first entry)
XX Human prostate-specific amino acid sequence P703P-DE14.
XX Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
XX chromosome 22q11.2; prostate-specific protein; chromosome 1;
XX

XX prostate specific antigen; PSA.
XX Homo sapiens.
XX WO200134802-A2.
XX 17-MAY-2001.
XX 09-NOV-2000; 2000WO-US030904.
XX 12-NOV-1999; 99US-00439313.
XX 18-NOV-1999; 99US-00443686.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
XX Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAM, Wang A;
XX WPI; 2001-308785/32.
XX Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer.
XX Claim 3; Page 188; 325pp; English.
XX The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production. The
CC polypeptides, nucleic acids and antibodies from the present invention are
CC useful in the diagnosis and therapy of prostate cancer. Prostate specific
CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic
CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
CC Prostate specific antigen (PSA) P501S was located on chromosome 1.
CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
CC and polypeptide sequences used in the exemplification of the present
CC invention
XX Sequence 164 AA;
SQ
Query Match 76.1%; Score 577; DB 4; Length 164;
Best Local Similarity 77.1%; Pred. No. 2,4e-46;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;
QY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGSGQWVEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGSGQWVEASLSVRHPEYN 60
QY 61 RPLLANDMLIKLDESVESDTRISISIASOCPAGNSCLVSGWGLANGELTGV----- 115
DB 61 RPLLANDMLIKLDESVESDTRISISIASOCPAGNSCLVSGWGLANGELTGV----- 115
QY 116 ----CLPSSRRSSAOSRGLTOSASQAECUPCC 144
DB 121 GMEWC-----EKLSPWOGCTISATSSAR-TSCC 148
RESULT 12
ABU71657 standard; protein; 164 AA.
XX ABU71657;
XX 10-JUN-2003 (first entry)
XX Prostate cancer specific antigen P703P #3.
XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
XX immunogen; cancer; prostate specific antigen.
XX Homo sapiens.
XX Synthetic.


```

XX  US2002192763-A1.
PN
XX
XX  19-DEC-2002.
PD
XX
XX  29-JUN-2001; 2001US-00895793.
PF
XX
XX  04-OCT-1999; 99US-0157455P.
PR  04-OCT-2000; 2000US-00679272.
PR  28-MAR-2001; 2001US-00828287.
XX
XX  (XU03/) XU J.
PA  (DILL/) DILLON D C.
PA  (MITC/) MITCHAM J L.
PA  (HARL/) HARLOCKER S L.
PA  (JIAN/) JIANG Y.
PA  (KALU/) KALOS M D.
PA  (FANG/) FANGER G R.
PA  (RETT/) RETTER M W.
PA  (STOL/) STOLK J A.
PA  (DAYC/) DAY C H.
PA  (VEDU/) VEDVICK T S.
PA  (CART/) CARTER D.
PA  (LISX/) LI S X.
PA  (WANG/) WANG A.
PA  (SKEI/) SKEIKY Y A W.
PA  (HEPL/) HEPLER M T.
PA  (HEND/) HENDERSON R A.
PA  (HURA/) HURAL J.
PA  (MCNE/) MCNEILL P D.
PA  (HOUN/) HOUGHTON R L.
PA  (DBAS/) Y DE BASSOLS C V.
PA  (FOYT/) FOY T M.
XX
XX  Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI  Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI  Li SX, Wang A, Skeiky YAW, Hepler MT, Henderson RA, Hural J;
PI  McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;
XX
XX  WPI; 2001-245062/25.
DR
XX
XX  Prostate specific protein and its encoding polynucleotide, useful for the
PT  treatment and diagnosis of prostate cancer.
XX
XX  Example 3; SEQ ID NO 178; 85pp; English.
PS
XX  The invention describes a fusion protein comprising at least one amino
CC  acid sequence of immunogenic portions of any of the 3 sequences not
CC  defined in the specification, or sequences having at least 70 or 90 %
CC  sequence identity to any one of the 3 sequences defined in the USPTO web
CC  site, which is encoded by any of the 4 nucleotide sequences not defined
CC  in the specification. The fusion protein, composition and methods are
CC  useful for diagnosing, preventing and/or treating cancer, particularly
CC  prostate cancer. The proteins are useful as markers to indicate the
CC  presence or absence of cancer. This is the amino acid sequence of a
CC  prostate cancer specific antigen. Note: The sequence data for this patent
CC  did not form part of the printed specification, but was obtained in
CC  electronic format directly from the US patent office at
XX  seqdata.uspto.gov/sequence.html?docID=US20020192763
XX
XX  Sequence 164 AA:
SQ
XX
XX  Query Match 76.1%; Score 577; DB 4; Length 164;
XX  Best Local Similarity 77.1%; Pred. No. 2,4e-46;
XX  Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;
XX
OY  1 MENELFCGVLVHPQWVLSAHCFOFNSYITGLGLHSLEADQPGSQMVEASLSVRHPEYN 60
DB  1 MENELFCGVLVHPQWVLSAHCFOFNSYITGLGLHSLEADQPGSQMVEASLSVRHPEYN 60
OY  61 RPLLANDMLIKLDESSESDDTIRTSISASOCPAGNSCLVSGWGLANGELTGV----- 115
DB  61 RPLLANDMLIKLDESSESDDTIRTSISASOCPAGNSCLVSGWGLANGELTGV----- 115
OY  19-JUL-2002 (first entry)
DB

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OY  116 -----CLPSSRRSSAQSRLTQSSASQAECCLPCC 144
DB  121 GGMWC-----EKLSPQMGCTISATSSAR-TSCC 148
XX
XX  RESULT 13
XX  AAU04965
XX  AAU04965 standard; protein; 164 AA.
XX
XX  AAU04965;
XX
XX  24-OCT-2001 (first entry)
XX
XX  Human prostate tumour protein DE14.
XX
XX  Human; prostate tumour protein; prostate cancer.
XX
XX  Homo sapiens.
XX
XX  US6262245-B1.
XX
XX  17-JUL-2001.
XX
XX  25-FEB-1998; 98US-00030607.
XX
XX  25-FEB-1997; 97US-00806099.
XX
XX  25-FEB-1997; 97US-00904804.
XX
XX  09-FEB-1998; 98US-00020956.
XX
XX  (CORI-) CORIXA CORP.
XX
XX  Xu J, Dillon DC;
XX
XX  WPI; 2001-440862/47.
XX
XX  N-PSDB; AAS10170.
XX
XX  Novel polynucleotide encoding polypeptide comprising a portion of
PT  prostate tumor protein useful for inhibiting development of prostate
PT  cancer or for treating prostate cancer in a patient.
XX
XX  Example 2; Col 176-177; 105pp; English.
PS
XX
XX  The sequence is a partial prostate tumour protein, encoded by a prostate
CC  tumour specific cDNA. The DNA is useful for inhibiting the development of
CC  prostate cancer or for treating prostate cancer in a patient
XX
XX  Sequence 164 AA:
SQ
XX
XX  Query Match 76.1%; Score 577; DB 4; Length 164;
XX  Best Local Similarity 77.1%; Pred. No. 2,4e-46;
XX  Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;
XX
OY  1 MENELFCGVLVHPQWVLSAHCFOFNSYITGLGLHSLEADQPGSQMVEASLSVRHPEYN 60
DB  1 MENELFCGVLVHPQWVLSAHCFOFNSYITGLGLHSLEADQPGSQMVEASLSVRHPEYN 60
OY  61 RPLLANDMLIKLDESSESDDTIRTSISASOCPAGNSCLVSGWGLANGELTGV----- 115
DB  61 RPLLANDMLIKLDESSESDDTIRTSISASOCPAGNSCLVSGWGLANGELTGV----- 115
OY  116 -----CLPSSRRSSAQSRLTQSSASQAECCLPCC 144
DB  121 GGMWC-----EKLSPQMGCTISATSSAR-TSCC 148
XX
XX  RESULT 14
XX  ABB95226
XX  ABB95226 standard; protein; 164 AA.
XX
XX  ABB95226;
XX
XX  19-JUL-2002 (first entry)
DB

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XX DE Human P703P-DE14 protein SEQ ID NO 178.
XX XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX KW gene therapy.
XX OS Homo sapiens.
XX PN US2002022248-A1.
XX PD 21-FEB-2002.
XX PF 12-JAN-2001; 2001US-00759143.
XX PR 25-FEB-1997; 97US-00806099.
XX PR 01-AUG-1997; 97US-00904804.
XX PR 10-FEB-1998; 98US-00020956.
XX PR 25-FEB-1998; 98US-00030607.
XX PR 14-JUL-1998; 98US-00115453.
XX PR 23-SEP-1998; 98US-00159812.
XX PR 15-JAN-1999; 99US-00232149.
XX PR 09-APR-1999; 99US-00288946.
XX PR 13-JUL-1999; 99US-00352616.
XX PR 12-NOV-1999; 99US-00439313.
XX PR 18-NOV-1999; 99US-00433686.
XX PR 14-JAN-2000; 2000US-00483672.
XX PR 27-MAR-2000; 2000US-00536857.
XX PR 09-MAY-2000; 2000US-00568100.
XX PR 12-MAY-2000; 2000US-00570737.
XX PR 13-JUN-2000; 2000US-00593793.
XX PR 27-JUN-2000; 2000US-00605783.
XX PR 10-AUG-2000; 2000US-00636215.
XX PR 29-AUG-2000; 2000US-00651236.
XX PR 06-SEP-2000; 2000US-00657279.
XX PR 02-OCT-2000; 2000US-00679426.
XX PR 10-OCT-2000; 2000US-00685166.
XX PA (XUUJ/) XU J.
XX PA (DILL/) DILLON D C.
XX PA (MITC/) MITCHAM J L.
XX PA (HARL/) HARLOCKER S L.
XX PA (JIAN/) JIANG Y.
XX PA (KALO/) KALOS M D.
XX PA (RANG/) RANGER G R.
XX PA (RETT/) RETTER M W.
XX PA (STOL/) STOLK J A.
XX PA (DAYC/) DAY C H.
XX PA (VEDV/) VEDVICK T S.
XX PA (CART/) CARTER D.
XX PA (LISX/) LI S X.
XX PA (WANG/) WANG A.
XX PA (SKEI/) SKEIKY Y A W.
XX PA (HEPL/) HEPLER W T.
XX PA (HEND/) HENDERSON R A.
XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
XX PI Fanger GR, Retter MW, Stoik JA, Day CH, Vedvick TS, Carter D;
XX PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX DR WPI; 2002-255649/30.
XX PT New prostate-specific polynucleotides for diagnosing and treating
XX PT diseases, in particular prostate cancer, and as markers for the
XX PT progression of cancer.
XX PS Claim 2; SEQ ID NO 178; 87bp; English.
XX CC The present invention provides prostate-specific coding sequences and
XX CC their encoded proteins. These can be used in the diagnosis and treatment
XX CC of cancers, particularly prostate cancer. The present sequence is a
XX CC protein described in the invention
XX SO Sequence 164 AA;

Query Match 76.1%; Score 577; DB 5; Length 164;
Best Local Similarity 77.1%; Pred. No. 2,4e-46;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;
QY 1 MENELFCGVLVHPQWVLSAHCPCFQNSYTTGLGLHSLEADQEPGSOVFEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAHCPCFQNSYTTGLGLHSLEADQEPGSOVFEASLSVRHPEYN 60
QY 61 RPLANDLMIKLDSESVESDITRISISIASQCPAGNSCLVSGWGLHANGELTGV----- 115
DB 61 RPLANDLMIKLDSESVESDITRISISIASQCPAGNSCLVSGWGLHANGELTGV----- 115
QY 116 ---CLPSSRRSSAQSRGLTQSSASQAECUPCC 144
DB 121 GWEC---EKLSPWOGCTTSATSSAR-TSCC 148
RESULT 15
ID ABG76669 standard; protein; 164 AA.
XX AC ABG76669;
XX DT 05-NOV-2002 (first entry)
XX DE Prostate tumour protein #7.
XX DE Prostate tumour; immunotherapy; prostate cancer.
XX KW Human; prostate tumour; immunotherapy; prostate cancer.
XX OS Homo sapiens.
XX PN US2002081580-A1.
XX PD 27-JUN-2002.
XX PR 25-FEB-1998; 98US-00030606.
XX PR 25-FEB-1997; 97US-00806596.
XX PR 01-AUG-1997; 97US-00904809.
XX PR 09-FEB-1998; 98US-00020747.
XX PA (XUUJ/) XU J.
XX PA (DILL/) DILLON D C.
XX PI Xu J, Dillon DC;
XX DR WPI; 2002-607662/65.
XX PT Detecting prostate cancer comprises contacting a sample with an agent
XX PT capable of binding to a polypeptide with an immunogenic portion of a
XX PT prostate protein, oligonucleotide primers or a probe specific for DNA
XX PT encoding the polypeptide.
XX PS Claim 1; Page 92; 11pp; English.
XX CC The invention relates to a method of detecting prostate cancer by
XX CC contacting a biological sample from a patient with: (a) a binding agent
XX CC that binds to a polypeptide having an immunogenic portion of a prostate
XX CC protein or its variant; (b) 2 oligonucleotide primers, where 1 of the
XX CC oligonucleotides is specific for a DNA encoding the polypeptide of (a);
XX CC or (c) an oligonucleotide probe specific for a DNA molecule encoding the
XX CC polypeptide of (a). The method and polypeptides are useful for
XX CC diagnosing, treating, particularly by immunotherapy, monitoring the
XX CC progression, and inhibiting the development of prostate cancer in a
XX CC patient. The polypeptides may be used to generate antibodies useful for
XX CC the diagnosis and monitoring of prostate cancer. ABG76663-ABG76669
XX CC represent human prostate tumour protein sequences of the invention
XX SO Sequence 164 AA;
Query Match 76.1%; Score 577; DB 5; Length 164;
Best Local Similarity 77.1%; Pred. No. 2,4e-46;

Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

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Qy 1 MENELFCGVLVHPQWVLSAHCFOFNSYTIIGLHSLPADQEPGSGQWYEASLSVRHPEYN 60
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Db 1 MENELFCGVLVHPQWVLSAHCFOFNSYTIIGLHSLPADQEPGSGQWYEASLSVRHPEYN 60
    |||||
Qy 61 RPLANDLMLIKLDESVESEDTRISISASQCPAGNSCLVSGWGLLANGEITGV----- 115
    |||||
Db 61 RPLANDLMLIKLDESVESEDTRISISASQCPAGNSCLVSGWGLLANGEITGV----- 120
    |||||
Qy 116 ----CLPSSRRSSAOSRGITQSSASQAECLPCC 144
    |||||
Db 121 GGMEC-----EKLSPWQGGCTISATSSAR-TSCC 148
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Search completed: August 29, 2006, 03:41:57
 Job time : 199 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 29, 2006, 03:59:14 ; Search time 176 Seconds
(without alignments)
384.258 Million cell updates/sec

Title: US-10-726-093-10

Perfect score: 758

Sequence: 1 MENELFCGVLVHPQWVLSA.....SRGLTOSASQAECPLCCSA 146

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA.Main.*
1: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US10_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	758	100.0	146	US-10-726-093-10	Sequence 10, Appl
2	758	100.0	195	US-10-473-485-2	Sequence 2, Appl
3	577	76.1	164	US-09-759-143-178	Sequence 178, App
4	577	76.1	164	US-09-780-669-178	Sequence 178, App
5	577	76.1	164	US-09-030-606-178	Sequence 178, App
6	577	76.1	164	US-09-822-827-178	Sequence 178, App
7	577	76.1	164	US-09-115-453-178	Sequence 178, App
8	577	76.1	164	US-09-232-880-178	Sequence 178, App
9	577	76.1	164	US-09-895-793-178	Sequence 178, App
10	577	76.1	164	US-09-895-814-178	Sequence 178, App
11	577	76.1	164	US-10-012-896-178	Sequence 178, App
12	577	76.1	164	US-10-010-940-178	Sequence 178, App
13	577	76.1	164	US-10-144-678A-178	Sequence 178, App
14	577	76.1	164	US-10-294-025-178	Sequence 178, App
15	577	76.1	164	US-10-688-838-178	Sequence 178, App
16	577	76.1	164	US-11-234-786-178	Sequence 178, App
17	577	76.1	205	US-10-726-093-8	Sequence 8, Appl
18	577	76.1	220	US-09-759-143-327	Sequence 327, App
19	577	76.1	220	US-09-780-669-327	Sequence 327, App
20	577	76.1	220	US-09-822-827-327	Sequence 327, App
21	577	76.1	220	US-09-232-880-327	Sequence 327, App
22	577	76.1	220	US-09-895-793-327	Sequence 327, App
23	577	76.1	220	US-09-895-814-327	Sequence 327, App
24	577	76.1	220	US-10-012-896-327	Sequence 327, App
25	577	76.1	220	US-10-010-940-327	Sequence 327, App
26	577	76.1	220	US-10-144-678A-327	Sequence 327, App
27	577	76.1	220	US-10-294-025-327	Sequence 327, App

28	577	76.1	220	US-11-234-786-327	Sequence 327, App
29	577	76.1	226	US-10-312-089-8	Sequence 8, Appl
30	577	76.1	254	US-09-759-143-525	Sequence 525, App
31	577	76.1	254	US-09-780-669-525	Sequence 525, App
32	577	76.1	254	US-09-822-827-525	Sequence 525, App
33	577	76.1	254	US-09-895-793-525	Sequence 525, App
34	577	76.1	254	US-09-895-814-525	Sequence 525, App
35	577	76.1	254	US-10-010-940-525	Sequence 525, App
36	577	76.1	254	US-10-144-678A-525	Sequence 525, App
37	577	76.1	254	US-10-312-089-7	Sequence 7, Appl
38	577	76.1	254	US-10-144-678A-525	Sequence 525, App
39	577	76.1	254	US-10-294-025-525	Sequence 525, App
40	577	76.1	254	US-10-473-485-6	Sequence 6, Appl
41	577	76.1	254	US-10-473-485-13	Sequence 13, Appl
42	577	76.1	254	US-11-234-786-525	Sequence 525, App
43	577	76.1	284	US-10-015-989A-54	Sequence 54, Appl
44	577	76.1	312	US-10-312-089-3	Sequence 3, Appl
45	577	76.1	344	US-09-822-827-973	Sequence 973, App

ALIGNMENTS

RESULT 1
US-10-726-093-10
Sequence 10, Application US/10726093
Publication No. US20050106643A1
GENERAL INFORMATION:
APPLICANT: Satecloglu, Fahri
TITLE OF INVENTION: Differentially Expressed Genes in
TITLE OF INVENTION: Prostate Cancer
FILE REFERENCE: 50218/002003
CURRENT APPLICATION NUMBER: US/10/726, 093
CURRENT FILING DATE: 2003-12-01
PRIOR APPLICATION NUMBER: US/09/743, 682
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: PCT/IB00/00673
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 60/135, 325
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: US 60/135, 333
PRIOR FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
US-10-726-093-10

Query Match 100.0%; Score 758; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.3e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENELFCGVLVHPQWVLSAHCFOFNSYITGILHSLDQEPGSGMVEASLSVRHPEVN 60
Db 1 MENELFCGVLVHPQWVLSAHCFOFNSYITGILHSLDQEPGSGMVEASLSVRHPEVN 60
QY 61 RPLANDLMLIKLDESVSSEDTRISISIASOCPAGNSCLVSGMGLANGELTGVCPLPS 120
Db 61 RPLANDLMLIKLDESVSSEDTRISISIASOCPAGNSCLVSGMGLANGELTGVCPLPS 120
QY 121 RRSASRGITOSASQAECPLCCSA 146
Db 121 RRSASRGITOSASQAECPLCCSA 146

RESULT 2
US-10-473-485-2
Sequence 2, Application US/10473485
Publication No. US20040137455A1
GENERAL INFORMATION:
APPLICANT: Clements, Judith A

```
APPLICANT: Dong, Ying
TITLE OF INVENTION: Polynucleotides and polypeptides linked to cancer and/or benign
FILE REFERENCE: DAVI172.004APC
CURRENT APPLICATION NUMBER: US/10/473,485
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: AU PR4022/01
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 195
TYPE: PRT
ORGANISM: human
US-10-473-485-2
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Query Match      100.0%; Score 758; DB 4; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.9e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 50 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 109
QY 61 RPLANDMLIKLDESVESEDTRISISASOCPFAGNSCLVSGWGLANGELTGVCLPSS 120
DB 110 RPLANDMLIKLDESVESEDTRISISASOCPFAGNSCLVSGWGLANGELTGVCLPSS 169
QY 121 RRSSAQRGLTQSSASQAECCLPCCSA 146
DB 170 RRSSAQRGLTQSSASQAECCLPCCSA 195
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RESULT 3

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US-09-759-143-178
Sequence 178, Application US/09759143
Patent No. US2002002248A1
GENERAL INFORMATION:
```

```
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 178
LENGTH: 164
TYPE: PRT
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(164)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-759-143-178
```

```
Query Match      76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 1e-54;
```

```
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;
```

```
QY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
QY 61 RPLANDMLIKLDESVESEDTRISISASOCPFAGNSCLVSGWGLANGELTGV----- 115
DB 61 RPLANDMLIKLDESVESEDTRISISASOCPFAGNSCLVSGWGLANDAVIAIQSXTV 120
QY 116 ----CLPSSRRSSAQRGLTQSSASQAECCLPCC 144
DB 121 GSWEC----EKLSQPWGCTTISATSSAR-TSCC 148
```

RESULT 4

```
US-09-780-669-178
Sequence 178, Application US/09780669
Patent No. US20020051977A1
GENERAL INFORMATION:
```

```
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 178
LENGTH: 164
TYPE: PRT
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(164)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-780-669-178
```

```
Query Match      76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 1e-54;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;
```

```
QY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
QY 61 RPLANDMLIKLDESVESEDTRISISASOCPFAGNSCLVSGWGLANGELTGV----- 115
DB 61 RPLANDMLIKLDESVESEDTRISISASOCPFAGNSCLVSGWGLANDAVIAIQSXTV 120
QY 116 ----CLPSSRRSSAQRGLTQSSASQAECCLPCC 144
DB 121 GSWEC----EKLSQPWGCTTISATSSAR-TSCC 148
```

RESULT 5

US-09-030-606-178
Sequence 178, Application US/09030606
Patent No. US20020081580A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS: BERRY LLP
ADDRESS: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/030.606
FILING DATE: 25-FEB-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C3

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 178:

SEQUENCE CHARACTERISTICS:

LENGTH: 164 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORGANISM: Homo sapiens

US-09-030-606-178

Query Match 76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 1e-54;

Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY 1 MENELFCGVLVHPQWVLSAHCFOFNSYTTIGLHSLLEADQEPGSGMVASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAHCFOFNSYTTIGLHSLLEADQEPGSGMVASLSVRHPEYN 60

QY 61 RPLANDLMLIKLDESSESDTIRISIASOCPAGNSCLVSGMGLANGELTGV----- 115
DB 61 RPLANDLMLIKLDESSESDTIRISIASOCPAGNSCLVSGMGLANGELTGV----- 115

QY 116 ----CLPSSRRSSAOSRGLTQSSASQAECPLCC 144
DB 121 GCWEC-----EKLSPMGCTISATSSAR-TSCC 148

RESULT 6

US-09-822-827-178

Sequence 178, Application US/09822827

Patent No. US20020081680A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.534C1

CURRENT APPLICATION NUMBER: US/09/822.827

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 178

LENGTH: 164

TYPE: PRT

ORGANISM: Homo sapien

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)...(164)

OTHER INFORMATION: Xaa = Any Amino Acid

US-09-822-827-178

Query Match 76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 1e-54;

Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY 1 MENELFCGVLVHPQWVLSAHCFOFNSYTTIGLHSLLEADQEPGSGMVASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAHCFOFNSYTTIGLHSLLEADQEPGSGMVASLSVRHPEYN 60

QY 61 RPLANDLMLIKLDESSESDTIRISIASOCPAGNSCLVSGMGLANGELTGV----- 115
DB 61 RPLANDLMLIKLDESSESDTIRISIASOCPAGNSCLVSGMGLANGELTGV----- 115

QY 116 ----CLPSSRRSSAOSRGLTQSSASQAECPLCC 144
DB 121 GCWEC-----EKLSPMGCTISATSSAR-TSCC 148

RESULT 7

US-09-115-453-178

Sequence 178, Application US/09115453B

Patent No. US20020090372A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, David C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND

FILE REFERENCE: 210121.427C4

CURRENT APPLICATION NUMBER: US/09/115.453B

CURRENT FILING DATE: 1998-07-14

NUMBER OF SEQ ID NOS: 228

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 178

LENGTH: 164

TYPE: PRT

ORGANISM: Homo sapien

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)...(164)

OTHER INFORMATION: Xaa = Any Amino Acid

US-09-115-453-178

Query Match 76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 1e-54;

Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY 1 MENELFCGVLVHPQWVLSAHCFOFNSYTTIGLHSLLEADQEPGSGMVASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAHCFOFNSYTTIGLHSLLEADQEPGSGMVASLSVRHPEYN 60

QY 61 RPLANDLMLIKLDESSESDTIRISIASOCPAGNSCLVSGMGLANGELTGV----- 115
DB 61 RPLANDLMLIKLDESSESDTIRISIASOCPAGNSCLVSGMGLANGELTGV----- 115

QY 116 ----CLPSSRRSSAOSRGLTQSSASQAECPLCC 144
DB 121 GCWEC-----EKLSPMGCTISATSSAR-TSCC 148

RESULT 8
US-09-232-880-178
Sequence 178, Application US/09232880
Publication No. US20020182596A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
FILE REFERENCE: 210121.428C6
CURRENT APPLICATION NUMBER: US/09/232,880
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 178
LENGTH: 164
TYPE: PRT
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(164)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-232-880-178

Query Match 76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 1e-54;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
QY 61 RPLANDMLIKLDSVSESDTIRISIASOCPAGNSCLVSGMGLANGELTGV----- 115
DB 61 RPLANDMLIKLDSVSESDTIRISIASOCPAGNSCLVSGMGLANGELTGV----- 120
QY 116 -----CLPSSRRSSAQSRGLTQSSASQAECPLPCC 144
DB 121 GGMWEC-----EKLSPWQCGCTISATSSAR-TSCC 148

RESULT 9

US-09-895-793-178
Sequence 178, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolck, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 178

LENGTH: 164
TYPE: PRT
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(164)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-895-793-178

Query Match 76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 1e-54;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
QY 61 RPLANDMLIKLDSVSESDTIRISIASOCPAGNSCLVSGMGLANGELTGV----- 115
DB 61 RPLANDMLIKLDSVSESDTIRISIASOCPAGNSCLVSGMGLANGELTGV----- 120
QY 116 -----CLPSSRRSSAQSRGLTQSSASQAECPLPCC 144
DB 121 GGMWEC-----EKLSPWQCGCTISATSSAR-TSCC 148

RESULT 10

US-09-895-814-178
Sequence 178, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolck, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 178
LENGTH: 164
TYPE: PRT
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(164)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-895-814-178

Query Match 76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 1e-54;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY 1 MENELFCGVLVHPQWVLSAHCFOHSYTTIGLGLHSLEADQEPGQWVEASLSVRHPEYN 60
| | | | |
Db 1 MENELFCGVLVHPQWVLSAHCFOHSYTTIGLGLHSLEADQEPGQWVEASLSVRHPEYN 60
| | | | |
QY 61 RPLANDMLIKLDESVESEDTRISISIASQCTAGNSCLVSGWGLLANGLTGV----- 115
| | | | |
Db 61 RPLANDMLIKLDESVESEDTRISISIASQCTAGNSCLVSGWGLLANGLTGV----- 115
| | | | |
QY 116 -----CLPSSRRSSAQSRLTQSSASQAECCLPCC 144
| | | | |
Db 121 GWECC-----EKLSPWQGGCTTISATSSAR-TSCC 148
| | | | |

RESULT 11

US-10-012-896-178
; Sequence 178, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 178
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 118
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-012-896-178

Query Match 76.1%; Score 577; DB 4; Length 164;
Best Local Similarity 77.1%; Pred. No. 1e-54;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;
QY 1 MENELFCGVLVHPQWVLSAHCFOHSYTTIGLGLHSLEADQEPGQWVEASLSVRHPEYN 60
| | | | |
Db 1 MENELFCGVLVHPQWVLSAHCFOHSYTTIGLGLHSLEADQEPGQWVEASLSVRHPEYN 60
| | | | |
QY 61 RPLANDMLIKLDESVESEDTRISISIASQCTAGNSCLVSGWGLLANGLTGV----- 115
| | | | |
Db 61 RPLANDMLIKLDESVESEDTRISISIASQCTAGNSCLVSGWGLLANGLTGV----- 115
| | | | |
QY 116 -----CLPSSRRSSAQSRLTQSSASQAECCLPCC 144
| | | | |

Db 121 GWECC-----EKLSPWQGGCTTISATSSAR-TSCC 148
| | | | |

RESULT 12

US-10-010-940-178
; Sequence 178, Application US/10010940
; Publication No. US20030088062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010.940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 178
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(164)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-010-940-178

Query Match 76.1%; Score 577; DB 4; Length 164;
Best Local Similarity 77.1%; Pred. No. 1e-54;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY 1 MENELFCGVLVHPQWVLSAHCFOHSYTTIGLGLHSLEADQEPGQWVEASLSVRHPEYN 60
| | | | |
Db 1 MENELFCGVLVHPQWVLSAHCFOHSYTTIGLGLHSLEADQEPGQWVEASLSVRHPEYN 60
| | | | |
QY 61 RPLANDMLIKLDESVESEDTRISISIASQCTAGNSCLVSGWGLLANGLTGV----- 115
| | | | |
Db 61 RPLANDMLIKLDESVESEDTRISISIASQCTAGNSCLVSGWGLLANGLTGV----- 115
| | | | |
QY 116 -----CLPSSRRSSAQSRLTQSSASQAECCLPCC 144
| | | | |
Db 121 GWECC-----EKLSPWQGGCTTISATSSAR-TSCC 148
| | | | |

RESULT 13

US-10-144-678A-178
; Sequence 178, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.

APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Hepler, William T.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Foy, Teresa M.
APPLICANT: Macanabe, Yoshihiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144, 678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 178
LENGTH: 164
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: 118
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-144-678A-178

Query Match 76.1%; Score 577; DB 4; Length 164;

Best Local Similarity 77.1%; Pred. No. 1e-54;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADDEPGSQMVEASISVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADDEPGSQMVEASISVRHPEYN 60
QY 61 RPLANDMLIKLDESVESEDPTIRISISIAOCPITAGNSCLVSGWGLLANGELTGV----- 115
DB 61 RPLANDMLIKLDESVESEDPTIRISISIAOCPITAGNSCLVSGWGLLANGELTGV----- 120
QY 116 ----CLPSSRRSSAOSRGLTQSSASQAECPLCC 144
DB 121 GGWEC----EKLSQPMQCTTISATSSAR-TSCC 148

RESULT 14

US-10-294-025-178

Sequence 178, Application US/10294025
Publication No. US20030185830A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Stolk, John A.

APPLICANT: Kalos, Michael D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.427C29

CURRENT APPLICATION NUMBER: US/10/294, 025

CURRENT FILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 1038

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 178

LENGTH: 164

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: VARIANT

LOCATION: 118

OTHER INFORMATION: Xaa = Any Amino Acid

US-10-294-025-178

Query Match 76.1%; Score 577; DB 4; Length 164;

Best Local Similarity 77.1%; Pred. No. 1e-54;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADDEPGSQMVEASISVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADDEPGSQMVEASISVRHPEYN 60
QY 61 RPLANDMLIKLDESVESEDPTIRISISIAOCPITAGNSCLVSGWGLLANGELTGV----- 115
DB 61 RPLANDMLIKLDESVESEDPTIRISISIAOCPITAGNSCLVSGWGLLANGELTGV----- 120
QY 116 ----CLPSSRRSSAOSRGLTQSSASQAECPLCC 144
DB 121 GGWEC----EKLSQPMQCTTISATSSAR-TSCC 148

RESULT 15

US-10-688-838-178

Sequence 178, Application US/10688838
Publication No. US20040141989A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, David C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

FILE REFERENCE: 210121.427D4

CURRENT APPLICATION NUMBER: US/10/688, 838

CURRENT FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 228

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 178

LENGTH: 164

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: VARIANT

LOCATION: 118

OTHER INFORMATION: Xaa = Any Amino Acid

US-10-688-838-178

Query Match 76.1%; Score 577; DB 4; Length 164;

Best Local Similarity 77.1%; Pred. No. 1e-54;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADDEPGSQMVEASISVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADDEPGSQMVEASISVRHPEYN 60
QY 61 RPLANDMLIKLDESVESEDPTIRISISIAOCPITAGNSCLVSGWGLLANGELTGV----- 115
DB 61 RPLANDMLIKLDESVESEDPTIRISISIAOCPITAGNSCLVSGWGLLANGELTGV----- 120
QY 116 ----CLPSSRRSSAOSRGLTQSSASQAECPLCC 144
DB 121 GGWEC----EKLSQPMQCTTISATSSAR-TSCC 148

Search completed: August 29, 2006, 04:05:40
Job time : 178 secs

Db 121 RRSASOGRGLTOSASQAECCLPCCSA 146

RESULT 2

096PT0_HUMAN PRELIMINARY; PRT; 195 AA.

ID 096PT0; Integrated into UniProtKB/TrEMBL.

DT 01-DEC-2001, sequence version 1.

DT 07-FEB-2006, entry version 24.

DE Kallikrein 4 splice variant.

GN Name=KLK4;

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

NCBI_TaxID=9606;

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=9367447; PubMed=10438493; DOI=10.1074/jbc.274.33.23210; Stephens S.A., Verity K., Ashworth L.K., Clements J.A.;

RA "Localization of a new prostate-specific antigen-related serine protease gene, KLK4, is evidence for an expanded human kallikrein gene family cluster on chromosome 19q13.3-13.4.";

RT J. Biol. Chem. 274:23210-23214 (1999).

RL J. Biol. Chem. 274:23210-23214 (1999).

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CC EMBL; AF148532; AL114782.1; -; Genomic_DNA.

DR HSSP; Q61955; INPM.

DR GO; GO:0008236; F:serine-type peptidase activity; ISS.

DR GO; GO:0006508; P:proteolysis; ISS.

DR InterPro; IPR001254; Peptidase_S1_S6.

DR InterPro; IPR001314; Peptidase_S1A.

DR Pfam; PF00089; Trypsin_1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR SMART; SM00020; TRYP_SPC; 1.

DR PROSITE; PS50240; TRYPsin_DOM; 1.

DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.

SQ SEQUENCE 195 AA; 20585 MW; EF7E96978B1515H1 CRC64;

Query Match 100.0%; Score 758; DB 2; Length 195;

Best Local Similarity 100.0%; Pred. No. 5.1e-66;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENELFCSGVLVHPQWVLSAHCFOVNSTYTGIGLHSLADQEPGQWVEASLSVHRPEYN 60

DB 50 MENELFCSGVLVHPQWVLSAHCFOVNSTYTGIGLHSLADQEPGQWVEASLSVHRPEYN 109

QY 61 RPLANDLMLIKLDESSESPTIRISISIASOCPTAGNSCLVSGMLANGELTGVCPLPS 120

DB 110 RPLANDLMLIKLDESSESPTIRISISIASOCPTAGNSCLVSGMLANGELTGVCPLPS 169

QY 121 RRSASOGRGLTOSASQAECCLPCCSA 146

DB 170 RRSASOGRGLTOSASQAECCLPCCSA 195

RESULT 3

096JDB_HUMAN PRELIMINARY; PRT; 131 AA.

ID 096JDB; Integrated into UniProtKB/TrEMBL.

DT 01-DEC-2001, sequence version 1.

DT 07-FEB-2006, entry version 20.

DE ARM1 (Fragment).

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Prostate;

RX MEDLINE=21398046; PubMed=11506707; DOI=10.1089/104454901750361497; Korkmaz K.S., Korkmaz C.G., Pretlow T.G., Saathigolu F.;

RA "Distinctly different gene structure of KLK4/KLK-L1/Protease/ARM1 compared with other members of the kallikrein family - Perinuclear localization, alternative CDNA forms and regulation by multiple hormones.";

RT DNA Cell Biol. 20:435-445 (2001).

RL DNA Cell Biol. 20:435-445 (2001).

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CC Distributed under the Creative Commons Attribution-NonDerivs license

CC EMBL; AF259968; AA017704.1; -; mRNA.

DR HSSP; Q61955; INPM.

DR Ensemble; ENSG00000167749; Homo sapiens.

DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.

DR GO; GO:0006508; P:proteolysis; IEA.

DR InterPro; IPR001254; Peptidase_S1_S6.

DR InterPro; IPR001314; Peptidase_S1A.

DR Pfam; PF00089; Trypsin_1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR SMART; SM00020; TRYP_SPC; 1.

DR PROSITE; PS50240; TRYPsin_DOM; 1.

DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.

FT NON_TER 131

SQ SEQUENCE 131 AA; 14107 MW; 03434B6D95AF2406 CRC64;

Query Match 76.1%; Score 577; DB 2; Length 131;

Best Local Similarity 96.5%; Pred. No. 1.8e-48;

Matches 111; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MENELFCSGVLVHPQWVLSAHCFOVNSTYTGIGLHSLADQEPGQWVEASLSVHRPEYN 60

DB 1 MENELFCSGVLVHPQWVLSAHCFOVNSTYTGIGLHSLADQEPGQWVEASLSVHRPEYN 60

QY 61 RPLANDLMLIKLDESSESPTIRISISIASOCPTAGNSCLVSGMLANGELTGVCPLPS 115

DB 61 RPLANDLMLIKLDESSESPTIRISISIASOCPTAGNSCLVSGMLANGELTGVCPLPS 115

RESULT 4

096JDB_HUMAN PRELIMINARY; PRT; 205 AA.

ID 096JDB; Integrated into UniProtKB/TrEMBL.

DT 01-DEC-2001, sequence version 1.

DT 07-FEB-2006, entry version 23.

DE ARM1.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX TISSUE=Prostate tumor xenograft;

RX MEDLINE=21398046; PubMed=11506707; DOI=10.1089/104454901750361497; Korkmaz K.S., Korkmaz C.G., Pretlow T.G., Saathigolu F.;

RA "Distinctly different gene structure of KLK4/KLK-L1/Protease/ARM1 compared with other members of the kallikrein family - Perinuclear localization, alternative CDNA forms and regulation by multiple hormones.";

RT DNA Cell Biol. 20:435-445 (2001).

RL DNA Cell Biol. 20:435-445 (2001).

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CC EMBL; AF259968; AA017704.1; -; mRNA.

DR HSSP; P00760; IEZX.

DR Ensemble; ENSG00000167749; Homo sapiens.

DR GO; GO:0008233; F:peptidase activity; IEA.

DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.

DR GO; GO:0006508; P:proteolysis; IEA.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PRO0722; CHYMOTRYPsin.
 DR SMART; SM00020; TRYPsin; 1.
 DR PROSITE; PS00240; TRYPsin; 1.
 DR PROSITE; PS00134; TRYPsin; 1.
 DR PROSITE; PS00135; TRYPsin; 1.
 DR Hydroxylase; Protease; Serine protease.
 KW SEQUENCE 205 AA; 21950 MW; B83A025C73DBA1F6 CRC64;
 SQ
 Query Match 76.1%; Score 577; DB 2; Length 205;
 Best Similarity 96.5%; Pident. No. 3.2e-48;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MENEELFCGSLVHPQWVLSAHCFOHSYTTGLGLHSLEADQEGSQWVEASISVRRPEVN 60
 DB 1 MENEELFCGSLVHPQWVLSAHCFOHSYTTGLGLHSLEADQEGSQWVEASISVRRPEVN 60
 QY 61 RPLLANDMLIKLDESVESDTRISISIASQCPAGNSCLVSGWGLANGELTGV 115
 DB 61 RPLLANDMLIKLDESVESDTRISISIASQCPAGNSCLVSGWGLANGELTGV 115
 RESULT 5
 KLU4_HUMAN STANDARD; PRT; 254 AA.
 ID KLU4_HUMAN
 AC Q9Y3F2; Q9GZL6; Q9UBU6;
 DT 01-DEC-2000; Integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1999; sequence version 1.
 DT 07-FEB-2006; entry version 44.
 DE Kallikrein-4 precursor (EC 3.4.21.-) (Protease) (Kallikrein-like
 DE protein 1) (KLU-L1) [Enamel matrix serine proteinase 1].
 GN Name=KLU4; Synonyms=EMSP1, PRSS17, PSTS;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=99413477; PubMed=10465467;
 RA Yousef G.M., Obiezu C.V., Luo L.-Y., Black M.H., Diamandis E.P.;
 RT "Prostate/KLU-L1 is a new member of the human kallikrein gene family,
 RT is expressed in prostate and breast tissues, and is hormonally
 RT regulated.";
 RL Cancer Res. 59:4252-4256(1999).
 RN NUCLEOTIDE SEQUENCE.
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99367447; PubMed=10438493; DOI=10.1074/jbc.274.33.23210;
 RA Stephenson S.A., Verity K., Ashworth L.K., Clements J.A.;
 RT "Localisation of a new prostate-specific antigen-related serine
 RT protease gene, KLU4, is evidence for an expanded human kallikrein
 RT family cluster on chromosome 19q13.3-13.4.";
 RL J. Biol. Chem. 274:23210-23214(1999).
 RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).
 RP PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
 RX Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
 RA Moss P., Paepker B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region.";
 RL Gene 257:119-130(2000).
 RN [5]

RP NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
 RX MEDLINE=20323211; PubMed=10863090; DOI=10.1016/S0378-1119(00)00203-1;
 RA Hu J.C.-C., Zhang C., Sun X., Yang Y., Cao X., Ryu O.-H., Stimmer J.P.;
 RT "Characterization of the mouse and human PRSS17 genes, their
 RT relationship to other serine proteases, and the expression of PRSS17
 RT in developing mouse incisors.";
 RL Gene 251:1-8(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC Tissue=prostatic carcinoma; Saetcioglu F.;
 RA Korkmaz K.S., Korkmaz C.G.,
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
 RX PubMed=15057824; DOI=10.1038/nature02399;
 RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
 RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
 RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
 RA Caenepeel S., Carrano A.V., Caole C., Chan Y.M., Christensen M.,
 RA Cleland C.A., Copeland A., Dalin E., Delal P., Denys M., Deter J.C.,
 RA Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,
 RA Glavina T., Gomez M., Gonzales E., Groza M., Hamon N., Hawkins T.,
 RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
 RA Kobayashi A., Lartionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
 RA Malatari S., Martinez D., McCreedy P.M., Medina C., Morgan J.,
 RA Nelson K., Nolan M., Ovcharenko I., Piatuck S., Pollard M.,
 RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
 RA Rodrigue A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
 RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
 RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
 RA Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
 RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
 RA Rubin E.M., Lucas S.M.;
 RT "The DNA sequence and biology of human chromosome 19.";
 RL Nature 428:529-535(2004).
 RN [8]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stappert M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pang C.C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millady S.J.,
 RA Bosa S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]
 RP NUCLEOTIDE SEQUENCE OF 22-254.
 RA Stimmer J.P., Ryu O.H., Qian Q., Zhang C., Cao X., Sun X., Hu C.-C.;
 RT "Cloning and characterization of a cDNA encoding human EMSP1.";
 RL (in) Goldberg M. (eds.);
 RL Chemistry and biology of mineralized tissues, pp. 1-1, American Academy
 RL of Orthopaedic Surgeons, Vitell (2000).
 CC -1- SUBCELLULAR LOCATION: Secreted protein.
 CC -1- TISSUE SPECIFICITY: Expressed in prostate.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 peptidase S1 domain.
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CC EMBL AF113140; AAD21580.1; -; mRNA.
DR EMBL AF113141; AAD21581.1; -; Genomic_DNA.
DR EMBL AF135023; AAD26424.2; -; Genomic_DNA.
DR EMBL AF145532; AAD38019.1; -; Genomic_DNA.
DR EMBL AF245527; AAG33357.1; -; Genomic_DNA.
DR EMBL AF228497; AAF70620.1; -; Genomic_DNA.
DR EMBL AF259699; AAF81227.1; -; mRNA.
DR EMBL AC037199; -; NOT ANNOTATED CDS; Genomic_DNA.
DR EMBL BC069325; AAH63325.1; -; mRNA.
DR EMBL BC069403; AAH69403.1; -; mRNA.
DR EMBL BC069429; AAH69429.1; -; mRNA.
DR EMBL BC069489; AAH69489.1; -; mRNA.
DR EMBL AF126401; AAG43246.1; -; mRNA.
DR HSSP_P00760; 1EXX.
DR MEROPS_S01_251; -.
DR Ensemble; ENSG00000167749; Homo sapiens.
DR HGNC; HGNC:6365; KLK4.
DR MIM; 603767; gene.
DR GO; GO:0005576; C:extracellular region; TAS.
DR GO; GO:0008236; F:serine-type peptidase activity; NAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SMO0020; TRYP_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR GlycoProtein; Hydrolyase; Protease; Serine protease; Signal; Zymogen.
KW SIGNAL
FT PROPEP 1 26
FT FT 27 30
FT FT 31 254
FT CHAIN 31 254
FT FT 31 252
FT DOMAIN 31 252
FT ACT_SITE 71 71
FT ACT_SITE 116 116
FT ACT_SITE 207 207
FT CARBOHYD 169 169
FT DISULFID 37 167
FT DISULFID 56 72
FT DISULFID 141 241
FT DISULFID 148 213
FT DISULFID 178 192
FT DISULFID 203 228
FT CONFLICT 197 197
FT SEQUENCE 254 AA; 27023 MW; 9C475E22B6E0C8 CRC64;

Query Match 76.1%; Score 577; DB 1; Length 254;
Best Local Similarity 96.5%; Pred. No. 4.1e-48;
Matches 111; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MENELFCGVLVHPQWVLSAAHCFQNSYITIGLGHSLFADDEPGSQMVEASLSVHPEYN 60
DB 50 MENELFCGVLVHPQWVLSAAHCFQNSYITIGLGHSLFADDEPGSQMVEASLSVHPEYN 109
QY 61 RPLANDLMLIKLDESSESPTIRSIASOCPTRAGNSCLVSGMGLANGELTGV 115
DB 110 RPLANDLMLIKLDESSESPTIRSIASOCPTRAGNSCLVSGMGLANGELTGV 164

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Maruina K., Farmer A.A., Rabin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman D.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (May-2005) to the EMBL/GenBank/DDBJ databases.
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-----
CC EMBL BC096178; AAH96178.1; -; mRNA.
CC EMBL BC096175; AAH96175.1; -; mRNA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SMO0020; TRYP_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease.
KW SEQUENCE 254 AA; 27023 MW; 9C475E22B6E0C8 CRC64;

Query Match 76.1%; Score 577; DB 2; Length 254;
Best Local Similarity 96.5%; Pred. No. 4.1e-48;
Matches 111; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MENELFCGVLVHPQWVLSAAHCFQNSYITIGLGHSLFADDEPGSQMVEASLSVHPEYN 60
DB 50 MENELFCGVLVHPQWVLSAAHCFQNSYITIGLGHSLFADDEPGSQMVEASLSVHPEYN 109
QY 61 RPLANDLMLIKLDESSESPTIRSIASOCPTRAGNSCLVSGMGLANGELTGV 115
DB 110 RPLANDLMLIKLDESSESPTIRSIASOCPTRAGNSCLVSGMGLANGELTGV 164

```

RESULT 6
O4VB16_HUMAN PRELIMINARY; PRT; 254 AA.
AC O4VB16;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Kallikrein 4, preproprotein.
GN Name=KLK4;
OS Homo sapiens (Human).

RESULT 7
O96RUS_HUMAN PRELIMINARY; PRT; 110 AA.
AC O96RUS;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 23.

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DE ARMI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
RN NCB1_TaxID=9606;
RX NUCLEOTIDE SEQUENCE.
RP MEDLINE=21398046; PubMed=11506707; DOI=10.1089/104454901750361497;
RA Korkmaz K.S., Korkmaz C.G., Prellow T.G., Saatchioglou F.;
RT "Distinctly different gene structure of KLK4/KLK-L1/Protease/ARMI
RT localized with other members of the kallikrein family - Perinuclear
RT localization, alternative cDNA forms and regulation by multiple
RT hormones.";
RL DNA Cell Biol. 20:435-445(2001).
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CC -----
DR HSSP; 061955; INPM.
DR Ensemble: ENSG00000167749; Homo sapiens.
CC GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN; 1.
SQ SEQUENCE 110 AA; 11858 MW; B6F9C135EA93B116 CRC64;

Query Match 75.7%; Score 574; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 2.9e-48;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENELFCGVLVHPQWVLSAHCFOFNSYTTGLGLHSLEADQPGSQWVEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAHCFOFNSYTTGLGLHSLEADQPGSQWVEASLSVRHPEYN 60

RESULT 8
Q96PT1_HUMAN PRELIMINARY; PRT; 159 AA.
ID Q96PT1_HUMAN
AC Q96PT1;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE Kallikrein 4 splice variant.
GN Name=KLK4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
RN NCB1_TaxID=9606;
RX NUCLEOTIDE SEQUENCE.
RP MEDLINE=99367447; PubMed=10438493; DOI=10.1074/jbc.274.33.23210;
RA Stephenson S.A., Verity K., Ashworth L.K., Clements J.A.;
RT "Localization of a new prostate-specific antigen-related serine
RT protease gene, KLK4, is evidence for an expanded human kallikrein gene
RT family cluster on chromosome 19q13-13.4.";
RL J. Biol. Chem. 274:23210-23214(1999).
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CC -----
DR EMBL; AF148532; AAL14781.1; -, Genomic_DNA.

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DR HSSP; 061955; INPM.
DR Ensemble: ENSG00000167749; Homo sapiens.
CC GO; GO:0008236; F:serine-type peptidase activity; ISS.
DR GO; GO:0006508; P:proteolysis; ISS.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN; 1.
SQ SEQUENCE 159 AA; 16931 MW; 3CC6BF491B6CA5A CRC64;

Query Match 75.7%; Score 574; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 4.6e-48;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENELFCGVLVHPQWVLSAHCFOFNSYTTGLGLHSLEADQPGSQWVEASLSVRHPEYN 60
DB 50 MENELFCGVLVHPQWVLSAHCFOFNSYTTGLGLHSLEADQPGSQWVEASLSVRHPEYN 109

QY 61 RPLANDLMLIKLDESSESPTIRSIASQCPAGNSCLVSGWGLANG 110
DB 110 RPLANDLMLIKLDESSESPTIRSIASQCPAGNSCLVSGWGLANG 159

RESULT 9
Q4VB17_HUMAN PRELIMINARY; PRT; 254 AA.
ID Q4VB17_HUMAN
AC Q4VB17;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Kallikrein 4, preproprotein.
GN Name=KLK4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
RN NCB1_TaxID=9606;
RX NUCLEOTIDE SEQUENCE.
RP TISSUE=PCR rescued clones;
RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klansner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Mulvaney S.J.,
RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulik S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Greenwood J., Smaila U., Smaila D.E.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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CC -----
CC Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

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DR EMBL: BC096177; AAH96177.1; -, mRNA.
DR GO: 0008233; F:peptidase activity; IEA.
DR GO: 0004252; F:serine-type endopeptidase activity; IEA.
DR GO: 0006508; P:proteolysis; IEA.
DR InterPro: IPR01254; Peptidase_S1_S6.
DR InterPro: IPR01314; Peptidase_S1A.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Hydrolase: Protease; Serine protease.
SQ SEQUENCE 254 AA; 27053 MW; 1C670B2B3BE5A5E CRC64;

Query Match 75.1%; Score 569; DB 2; Length 254;
Best Local Similarity 95.7%; Pred. No. 2, 5e-47;
Matches 110; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MENELFCGVLVHPQWLSAAHCFQNSYTTIGLHSLSEADQEPGQWVEASLSVRHPEYN 60
Db 50 MENELFCGVLVHPQWLSAAHCFQNSYTTIGLHSLSEADQEPGQWVEASLSVRHPEYN 109
61 RPLANDLMLIKLDESSESDDTIRISIASQCPTAGNSCLVSGWGLLANGELTGV 115
110 RPLANDLMLIKLDESSESDDTIRISIASQCPTAGNSCLVSGWGLLANGRMPTV 164

RESULT 10
096JEL_HUMAN PRELIMINARY; PRT; 205 AA.
AC 096JEL;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE ARM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=21398046; PubMed=11506707; DOI=10.1089/104454901750361497;
RA Korkmaz K.S., Korkmaz C.G., Preclow T.G., Saaticoglu F.;
RT "Distinctly different gene structure of KLK4/KLK-L1/Protease/ARM1
RT compared with other members of the kallikrein family - Perinuclear
RT localization, alternative cDNA forms and regulation by multiple
RT hormones."
RL DNA Cell Biol. 20:435-445(2001).
CC -----
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CC -----
DR EMBL: AF259964; AAK71701.1; -, mRNA.
DR HSSP: P00760; IEZX.
DR Ensemble: ENSG00000167749; Homo sapiens.
DR GO: 0008233; F:peptidase activity; IEA.
DR GO: 0004252; F:serine-type endopeptidase activity; IEA.
DR GO: 0006508; P:proteolysis; IEA.
DR InterPro: IPR01254; Peptidase_S1_S6.
DR InterPro: IPR01314; Peptidase_S1A.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Hydrolase: Protease; Serine protease.
SQ SEQUENCE 205 AA; 22052 MW; 159B61A20D94BD57 CRC64;

Query Match 74.7%; Score 566; DB 2; Length 205;
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Best Local Similarity 94.8%; Pred. No. 3, 8e-47;
Matches 109; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MENELFCGVLVHPQWLSAAHCFQNSYTTIGLHSLSEADQEPGQWVEASLSVRHPEYN 60
Db 1 MENELFCGVLVHPQWLSAAHCFQNSYTTIGLHSLSEADQEPGQWVEASLSVRHPEYN 60
61 RPLANDLMLIKLDESSESDDTIRISIASQCPTAGNSCLVSGWGLLANGELTGV 115
61 RPLANDLMLIKLDESSESDDTIRISIASQCPTAGNSCLVSGWGLLANGRMPTV 115

RESULT 11
096JEL_HUMAN PRELIMINARY; PRT; 204 AA.
AC 096JEL;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE ARM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=21398046; PubMed=11506707; DOI=10.1089/104454901750361497;
RA Korkmaz K.S., Korkmaz C.G., Preclow T.G., Saaticoglu F.;
RT "Distinctly different gene structure of KLK4/KLK-L1/Protease/ARM1
RT compared with other members of the kallikrein family - Perinuclear
RT localization, alternative cDNA forms and regulation by multiple
RT hormones."
RL DNA Cell Biol. 20:435-445(2001).
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CC -----
DR EMBL: AF259965; AAK71701.1; -, mRNA.
DR HSSP: P00760; IEZX.
DR Ensemble: ENSG00000167749; Homo sapiens.
DR GO: 0008233; F:peptidase activity; IEA.
DR GO: 0004252; F:serine-type endopeptidase activity; IEA.
DR GO: 0006508; P:proteolysis; IEA.
DR InterPro: IPR01254; Peptidase_S1_S6.
DR InterPro: IPR01314; Peptidase_S1A.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Hydrolase: Protease; Serine protease.
SQ SEQUENCE 204 AA; 21811 MW; 45742165D23A5F3 CRC64;

Query Match 74.0%; Score 561; DB 2; Length 204;
Best Local Similarity 96.2%; Pred. No. 1, 2e-46;
Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MENELFCGVLVHPQWLSAAHCFQNSYTTIGLHSLSEADQEPGQWVEASLSVRHPEYN 60
Db 1 MENELFCGVLVHPQWLSAAHCFQNSYTTIGLHSLSEADQEPGQWVEASLSVRHPEYN 60
61 RPLANDLMLIKLDESSESDDTIRISIASQCPTAGNSCLVSGWGLLANG 110
61 RPLANDLMLIKLDESSESDDTIRISIASQCPTAGNSCLVSGWGLLANG 110

RESULT 12
09XSN6_PIG PRELIMINARY; PRT; 254 AA.
AC 09XSN6;
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DR 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DR 01-NOV-1999, sequence version 1.
DR 07-FEB-2006, entry version 31.
DE Enamel matrix serine proteinase 1 precursor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
CC NCBI_TaxID=9823;
CC [1]
CC NUCLEOTIDE SEQUENCE.
CC MEDLINE=98126310; PubMed=9465170;
CC Simer J.P., Fukae M., Tanabe T., Yamakoshi Y., Uchida T., Xue J.,
CC Margolis H.C., Shimizu M., DeHart B.C., Hu C.-C., Bartlett J.D.,
CC "Purification, characterization, and cloning of enamel matrix serine
CC proteinase 1".
CC J. Dent. Res. 77:377-386(1998).
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CC -----
DR EMBL: U76256; AAB94638.1; -, mRNA.
DR HSP: P00760; IEZX.
DR MEROPS: S01.251; -.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO: GO:0006508; P:proteolysis; IEA.
DR InterPro: IPR001254; Peptidase_S1_S6.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00089; Trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PS0240; TRYPsin DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
DR Hydroxylase; Protease; Serine protease; Signal.
DR SIGNAL 1
DR CHAIN 1 254 enamel matrix serine proteinase 1.
DR SEQUENCE 254 AA; 27235 MW; FD40EF8564406F1 CRC64;
SQ
Query Match 63.6%; Score 482; DB 2; Length 254;
Best Local Similarity 76.5%; Pred. No. 8.8e-39;
Matches 88; Conservative 14; Mismatches 13; Indels 0; Gaps 0;
QY 1 MENELFCGVLVHPQWLSAHCFOHSYITGLGHSLEADQEGSGQWVEASLSVRPEYN 60
DB 50 LEEDFCGVLVHPQWLSAHCFOHSYITGLGHSLEADQEGSGQWVEASLSVRPEYN 109
QY 61 RPLANDMLIKLDESVESEDTRISISIASQCTAGNSCLVSGWGLLANGEITGV 115
DB 110 EFSMADMLIKLKESEVSLSDTVANISVSGCPTGDSCLVSGWGLRSLDQV 164
RESULT 13
Q6IE12.RAT PRELIMINARY; PRT; 256 AA.
AC Q6IE12
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 15.
DE Kallikrein 4 precursor.
GN Name=K14;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
CC [1]
CC NUCLEOTIDE SEQUENCE.
CC STRAIN=Sprague-Dawley;
CC PubMed=15060002; DOI=10.1101/gr.1946104;
CC Puente X.S., Lopez-Otin C.;
RT "A genomic analysis of rat proteases and protease inhibitors.";

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RL Genome Res. 14:609-622(2004).
CC -I- MICELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
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CC -----
DR EMBL: BN000381; CAE51907.1; -, mRNA.
DR HSP: P00761; IAKS.
DR Ensemble; ENSRNOG0000018864; Rattus norvegicus.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO: GO:0006508; P:proteolysis; IEA.
DR InterPro: IPR001254; Peptidase_S1_S6.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00089; Trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PS0240; TRYPsin DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
DR Hydroxylase; Protease; Serine protease; Signal.
DR SIGNAL 1
DR CHAIN 1 30 Kallikrein 4.
DR SEQUENCE 256 AA; 27925 MW; 8860B9153DB3285 CRC64;
SQ
Query Match 59.1%; Score 448; DB 2; Length 256;
Best Local Similarity 65.9%; Pred. No. 1.9e-35;
Matches 85; Conservative 16; Mismatches 26; Indels 2; Gaps 1;
QY 2 ENELFCGVLVHPQWLSAHCFOHSYITGLGHSLEADQEGSGQWVEASLSVRPEYN 61
DB 53 DNAPFCGVLVHPQWLSAHCFOHSYITGLGHSLEADQEGSGQWVEASLSVRPEYN 112
QY 62 RPLANDMLIKLDESVESEDTRISISIASQCTAGNSCLVSGWGLLANGEITGV--CLPS 119
DB 113 PEFANDMLIKLKESEVSLSDTVANISVSGCPTGDSCLVSGWGLRSLDQV 172
QY 120 SRSSASQR 128
DB 173 SVASEETCR 181
RESULT 14
Q9JIS2.MOUSE PRELIMINARY; PRT; 255 AA.
AC Q9JIS2
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 31.
DE Enamel matrix serine proteinase 1 precursor.
GN Name=K14; Synonyms=Prss17;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
CC [1]
CC NUCLEOTIDE SEQUENCE.
CC STRAIN=129/SvJ;
CC MEDLINE=20323211; PubMed=10863090; DOI=10.1016/S0378-1119(00)00203-1;
CC Hu J.C.-C., Zhang C., Sun X., Yang Y., Cao X., Ryu O., Simer J.P.;
CC "Characterization of the mouse and human PRSS17 genes, their
CC relationship to other serine proteases, and the expression of PRSS17
CC in developing mouse incisors.";
CC Gene 251:1-8(2000).
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CC -----
DR EMBL: AF198031; AAF85937.1; -, Genomic DNA.
DR HSP: P00760; IEZX.
DR MEROPS: S01.251; -.

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DR Ensembl; ENSMUSG0000006948; Mus musculus.
 DR MGI; MGI:1861379; K1k4.
 DR GO; GO:0005615; Cytochrome c; Cytosolic space; RCA.
 DR GO; GO:0004263; F-tyrosinase activity; RCA.
 DR GO; GO:0004295; F-tyrosinase activity; RCA.
 DR GO; GO:000508; P-proteinase; RCA.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYPSIN_DOM; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR KEGG; K04491; Serine protease; Signal.
 DR SIGNAL 1 25
 FT CHAIN 32 255
 SQ SEQUENCE 255 AA; 27536 MW; 6BFBFA7DAD679C CRC64;

Query Match 56.9%; Score 431; DB 2; Length 255;
 Best Local Similarity 63.6%; Pred. No. 9e-34;
 Matches 82; Conservative 18; Mismatches 27; Indels 2; Gaps 1;

QY 2 ENELPSCGVLVHPQWLSAHCFCNSYITGLGHSLEADQEPSCQWVEASLSVRHPEVNR 61
 DB 52 EDGFCGVLVHPQWLSAHCFCNSYITGLGHSLEADQEPSCQWVEASLSVRHPEVNR 111
 QY 62 PLIANDMLIKIDESVSDTIRISISASQCTPAGNSCLVSGWGLANGELNGV--CLPS 119
 DB 112 PSFANDMLIKINESVSDTIRISIVATQCTPPTCLVSGWGLKNGKLPGLQCNVL 171
 QY 120 SRRSSAQR 128
 DB 172 SVASEETCR 180

RESULT 15
 Q9Z0M1_MOUSE PRELIMINARY; PRT; 255 AA.
 AC Q9Z0M1;
 DT 01-MAY-1999; Integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1999; sequence version 1.
 DT 07-FEB-2006; entry version 36.
 DE Enamel matrix serine proteinase 1 precursor (Kallikrein 4) (Protease, enamel matrix, prostatic).
 GN Name=K1k4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Swiss-Webster;
 RX MEDLINE=20232321; PubMed=10663090; DOI=10.1016/S0378-1119(00)00203-1;
 RA Hu J.C.-C., Zhang C., Sun X., Yang Y., Cao X., Ryu O., Simmer J.P.;
 RT "Characterization of the mouse and human PRSS17 genes, their relationship to other serine proteases, and the expression of PRSS17 in developing mouse incisors";
 RL Gene 251:1-8(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Swiss-Webster;
 RX MEDLINE=20152522; PubMed=10690663;
 RA Hu J.C.-C., Ryu O.H., Chen J.J., Uchida T., Wakita K., Murakami C., Jiang H., Qian Q., Zhang C., Ottmers V., Bartlett J.D., Simmer J.P.;
 RT "Localization of Emspi expression during tooth formation and cloning of mouse cDNA."; Dent. Res. 79:70-76(2000).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Swiss-Webster;
 RA Simmer J.P.

RT "Enamel Matrix Serine Proteinase 1 (EMSP1)";
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Scheeter C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marustina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Cantin P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RG NIH MGC Project;
 RL Submitted (Aug-2005) to the EMBL/GenBank/DBJ databases.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonCommercial license
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 DR EMBL; AF019979; AAC98894.1; -; mRNA.
 DR EMBL; BC100717; AA100718.1; -; mRNA.
 DR EMBL; BC100718; AA100719.1; -; mRNA.
 DR EMBL; BC100716; AA100717.1; -; mRNA.
 DR EMBL; BC100719; AA100720.1; -; mRNA.
 DR HSP; P00760; 1EXZ.
 DR MEROPS; S01.251; -.
 DR Ensembl; ENSMUSG0000006948; Mus musculus.
 DR MGI; MGI:1861379; K1k4.
 DR GO; GO:0005615; Cytochrome c; Cytosolic space; RCA.
 DR GO; GO:0004263; F-tyrosinase activity; RCA.
 DR GO; GO:0004295; F-tyrosinase activity; RCA.
 DR GO; GO:000508; P-proteinase; RCA.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYPSIN_DOM; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR KEGG; K04491; Serine protease; Signal.
 DR SIGNAL 1 25
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 DB 112 PSFANDMLIKINESVSDTIRISIVATQCTPPTCLVSGWGLKNGKLPGLQCNVL 171

Qy	120	SRSSAOSR	128
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Search completed: August 29, 2006, 03:47:02
Job time : 302 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 28, 2006, 18:09:34 ; Search time 3295 Seconds
(without alignments)
4250.223 Million cell updates/sec

Title: US-10-726-093-10

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying Chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	758	100.0	702	2	AX052869 Sequence
2	758	100.0	702	5	AF259970 Homo sapi
3	758	100.0	1265	2	BD070317 Compounds

4	758	100.0	1265	2	BD242081
5	758	100.0	1265	2	AR237264
6	758	100.0	1265	2	AR278288
7	758	100.0	1265	2	AR366984
8	758	100.0	1265	2	AR370880
9	758	100.0	1265	2	AR392385
10	758	100.0	1265	2	AR400020
11	758	100.0	1265	2	AR439491
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13	758	100.0	1265	2	AR588653
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17	758	100.0	1265	2	AR716719
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21	758	100.0	1265	2	AX267199
22	758	100.0	1265	2	AX052876
23	730	96.3	701	2	AX969474
24	695	91.7	484	2	BD108193
25	695	91.7	484	2	AR412640
26	695	91.7	4385	5	AF148532
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29	660	87.1	7115	5	AF228497
30	660	87.1	40466	12	AC135047
31	660	87.1	217346	12	AC027602
32	660	87.1	230000	5	AC01483
33	660	86.0	107487	5	BD070318
34	652	86.0	1459	2	BD242082
35	640	84.4	1459	2	AR237265
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41	640	84.4	1459	2	AR405288
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RESULT 1	AX052869	702 bp	DNA	linear	PAT 12-JAN-2001
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DEFINITION	Sequence 3 from Patent WO0071711.				
ACCESSION	AX052869				
VERSION	AX052869.1	GI:12226978			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Homnidae; Homo.				
REFERENCE					
AUTHORS	Saatioglu, F.				
TITLE	Differentially expressed genes in prostate cancer				
JOURNAL	Patent: WO 0071711-A 3 30-NOV-2000;				
	Saatioglu, Fahri (NO)				
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Pred. No.: 758.00 Matches: 146

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Percent Similarity: 100.0%
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Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-726-093-10 (1-146) x AX052869 (1-702)

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QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
Db 61 GCACACGTGTTCCAGAACTCCTACACCATCGGCTGGGCTGCACAGCTTGGAGCCGAC 120
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60
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Db 181 AGACCTTCTGCTCGCTAACGACCTCATGCTCATCAAGTTGAGCAGATCCGTGCGAGTCT 240
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Db 241 GACACCATCCGAGCATCAGCATGCTTCCGAGTGCCCTACCGCGGGAACTTGGCTC 300
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
Db 301 GTTTCGTGGCTGGGCTCTGCTGCGAACGCTGACGAGGTGTGTCTCCCTCTTCA 360
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
Db 361 AGGAGTCTCTGCGCCATGCTCGGGGGCTGACCCAGACCTCGCTGCCAGCAGAAATGC 420
QY 141 LeuProCysCysSerAla 146
Db 421 CTACCGTCTGTCAGTGC 438
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RESULT 2
LOCUS AF259970 702 bp mRNA linear PRI 02-AUG-2001
DEFINITION Homo sapiens ARM1 mRNA, alternatively spliced, complete cds.
ACCESSION AF259970
VERSION AF259970.1 GI:14646878
KEYWORDS

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 702)
Korkmaz, K.S., Korkmaz, C.G., Pretlow, T.G. and Saetcioglu, F.
Distinctly Different Gene Structure of KLK4/KLK-11/Prostate/ARM1
Compared with Other Members of the Kallikrein Family: Intracellular
Localization, Alternative CDNA Forms, and Regulation by Multiple
Hormones
DNA Cell Biol. 20 (7), 435-445 (2001)

JOURNAL PUBMED 11506707
REFERENCE 2 (bases 1 to 702)
AUTHORS Korkmaz, K.S., Korkmaz, C.G. and Saetcioglu, F.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2000) Biotechnology Center of Oslo, University of
Oslo, Gaustadalleen 21, Oslo 0349, Norway
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Location/Qualifiers
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recorded"

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ORIGIN

Alignment Scores:
Pred. No.: 5,3e-65 Length: 702
Score: 758.00 Matches: 146
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Best Local Similarity: 100.0% Mismatch: 0
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US-10-726-093-10 (1-146) x AF259970 (1-702)

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QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
Db 361 AGGAGTCTCTGCGCCATGCTCGGGGGCTGACCCAGACCTCGCTGCCAGCAGAAATGC 420
QY 141 LeuProCysCysSerAla 146
Db 421 CTACCGTCTGTCAGTGC 438
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RESULT 3
LOCUS BD070317 1265 bp DNA linear PAT 27-AUG-2002
DEFINITION Compounds for immunodiagnosis of prostate cancer and methods for
their use.
ACCESSION BD070317
VERSION BD070317.1 GI:22615920
KEYWORDS JP 2001513886-A/168.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1265)
Xu, J. and Dillon, D.C.
Compounds for immunodiagnosis of prostate cancer and methods for
their use
Patent: JP 2001513886-A 168 04-SEP-2001;
CORIXA CORP
OS Homo sapiens (human)
PN JP 2001513886-A/168

JOURNAL
TITLE
AUTHORS
COMMENT

PD 04-SEP-2001
 PF 25-FEB-1998 JP 1998537008
 PR 25-FEB-1997 US 08/806596.01-AUG-1997 US 08/904809 PR
 09-FEB-1998 US 09/020747
 PI JIANGCHUN XU DAVIN C DILLON
 PC GOIN33/574,GOIN33/577,C07K16/30,A61K39/395,A61K47/48,C12Q1/68,
 PC GOIN33/543
 CC Strandedness: Single;
 CC Topology: Linear;
 CC Compounds for immunodiagnosis of prostate cancer and methods
 for their use
 CC Key Location/Qualifiers
 FT source 1..1265
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 Query Match: 100.0% Indels: 0
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US-10-726-093-10 (1-146) x BD070317 (1-1265)

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 DB 160 CAAAGCCAGGAGCCAGATGTTGAGGCCACTCTCCCTACGGCACCAGAGTACAAAC 219
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 DB 340 GTTTCGGCTGGGCTCTGCTGGGACAGGTGAGCTCAGGGTGTGTCTGCCCTCTTCA 399
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
 DB 400 AGAGAGTCTCTGCTCCAGCTCGCGGGGCTGACCCAGAGCTCTGCTCCAGAGATGC 459
 QY 141 LeuProCysCysSerAla 146
 DB 460 CTACCGTGTGACGATGCG 477

RESULT 4

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 LOCUS BD242081
 DEFINITION Compounds for immunotherapy and diagnosis of prostate cancer and
 methods for their use.

ACCESSION BD242081
 VERSION BD242081.1 GI:33051851
 KEYWORDS UP 2002520054-A/168.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Homnidae; Homo
 1 (bases 1 to 1265)
 DILLON,D.C., HARLOCKER,S.L., YUQIU,J., XU,J. and MITCHAM,J.L.
 Compounds for immunotherapy and diagnosis of prostate cancer and
 methods for their use
 Parent: JP 2002520054-A 168 09-JUL-2002;
 JOURNAL CORIXA CORP
 OS Homo sapiens (human)
 PN JP 2002520054-A/168
 PD 09-JUL-2002
 PF 14-JUL-1999 JP 2000560247
 PR 14-JUL-1998 US 09/115453,14-JUL-1998 US 09/116134 PR
 23-SEP-1998 US 09/159822,23-SEP-1998 US 09/159812 PR
 15-JAN-1999 US 09/232880,15-JAN-1999 US 09/232149 PR
 09-APR-1999 US 09/288946
 PI DAVIN CLIFFORD DILLON,SUSAN LOUISE HARLOCKER,JIANG YUQIU, PI
 JIANGCHUN XU,
 PI JENNIFER LYNN MITCHAM

COMMENT

PC C12N15/09,A61K38/00,A61K39/00,A61K39/395,C07K14/47,C07K16/30,
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 Best Local Similarity: 100.0% Mismatches: 0
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 DB: 2 Gaps: 0

US-10-726-093-10 (1-146) x BD242081 (1-1265)

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 DB 160 CAAAGCCAGGAGCCAGATGTTGAGGCCACTCTCCGTACGGCACCAGAGTACAAAC 219
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 DB 220 AGACCTTGTGCTTAACGACCTCATGCTCATCAAGTGGACGAATCCGTGTCGAGTCT 279
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
 DB 280 GACACCATCCGAGGACATCAGCAATGCTTCCAGAGCCCTACCGGGGGAACCTTGCTTC 339
 QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
 DB 340 GTTTCGGCTGGGCTCTGCTGGGACAGGTGAGCTCAGGGTGTGTCTGCCCTCTTCA 399
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
 DB 400 AGAGAGTCTCTGCTCCAGCTCGCGGGGCTGACCCAGAGCTCTGCTCCAGAGATGC 459

OY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCGAGTGGC 477

RESULT 5
LOCUS AR337264 1265 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 173 from patent US 6465611.
ACCESSION AR337264
VERSION AR337264.1 GI:27281922
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1265)
AUTHORS Xu,J., Dillon,D.C. and Mitcham,J.L.
TITLE Compounds for immunotherapy of prostate cancer and methods for their use
JOURNAL Patent: US 6465611-A 173 15-OCT-2002;
Corixa Corporation; Seattle, WA

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Location/Qualifiers
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Pred. No.: 9,47e-65 Length: 1265
Score: 758.00 Matches: 146
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DB 100 GCACACTGTTTCCAGAACTCTACACCATCGGGCTGGGCTGCACAGTCTTGAGCCGAC 159

OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTrpAsn 60
DB 160 CAAGAGCCAGGAGGAGCCAGATGGTGAGGCGACCTCTCCGTACGGCACCAGATACAC 219

OY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGTCTGCTACGACCTCATGCTCATCAAGTTGAGAGATCCGTGCCAGTCT 279

OY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGCATCGACTTCTCTTCCAGTCCCTTACCGGGGAACTCTTGCTTC 339

OY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGTGCTGGGCTGCTGTCGCAACGCTGAGCTCACGGGTGTGTCTGCCCTTCA 399

OY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGluAlaGluCys 140
DB 400 AGAGAGTCTCTGCGCCAGTCCGGGGGCTGACCCAGAGCTCTGCTCCAGGACAGATGC 459

OY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCGAGTGGC 477

RESULT 6
LOCUS AR278288 1265 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 173 from patent US 6512094.
ACCESSION AR278288

VERSION AR278288.1 GI:29712534
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1265)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W., Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6512094-A 173 28-JAN-2003;
Corixa Corporation; Seattle, WA

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Location/Qualifiers
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ORIGIN
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Pred. No.: 9,47e-65 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-726-093-10 (1-146) x AR278288 (1-1265)

OY 1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAGCGAATTGTTCTGCTGGGCGTCTGTCGATCCGACGTGGGTGCTGCACGC 99

OY 21 AlaHisCysPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACTCTACACCATCGGGCTGGGCTGCACAGTCTTGAGCCGAC 159

OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTrpAsn 60
DB 160 CAAGAGCCAGGAGGAGCCAGATGGTGAGGCGACCTCTCCGTACGGCACCAGATACAC 219

OY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGTCTGCTACGACCTCATGCTCATCAAGTTGAGAGATCCGTGCCAGTCT 279

OY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGCATCGACTTCTCTTCCAGTCCCTTACCGGGGAACTCTTGCTTC 339

OY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGTGCTGGGCTGCTGTCGCAACGCTGAGCTCACGGGTGTGTCTGCCCTTCA 399

OY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGluAlaGluCys 140
DB 400 AGAGAGTCTCTGCGCCAGTCCGGGGGCTGACCCAGAGCTCTGCTCCAGGACAGATGC 459

OY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCGAGTGGC 477

RESULT 7
LOCUS AR366984 1265 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 173 from patent US 6329505.
ACCESSION AR366984
VERSION AR366984.1 GI:34599959
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1265)

AUTHORS

Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Yugiu, J.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A. and
Day, C.H.

TITLE

Compositions and methods for therapy and diagnosis of prostate
cancer

JOURNAL

Patent: US 6329505-A 173 11-DEC-2001;
Corixa Corporation; Seattle, WA

FEATURES

Location/Qualifiers
1..1265
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
9.47e-65	1265	146	0	0	0	0
Percent Similarity:	100.0%					
Best Local Similarity:	100.0%					
Query Match:	100.0%					

US-10-726-093-10 (1-146) x AR366984 (1-1265)

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OY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValIleuSerAla 20
DB 40 ATGGAACAGAAATGTTCTGCTCGGCGCTCGTGCATCCGACATGGAGTGTCTGACGCC 99
OY 21 AlaHisCysPheGlnAsnSerTyrrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCAGAACTCTTACACCTCCTGAGCTGGAGCTGAGCTGAGCTGAGCTGAG 159
OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60
DB 160 CAAAGCCAGGAGGAGCAGATGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 219
OY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGTCTGCTTACACCTCCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 279
OY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGGAGCATGACATGCTTGTGCGAGTGCATCCGCGGAGAACTTTGCCCTC 339
OY 101 ValSerGlyTyrPglYLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTTCGTGCTGGGCTGCTGCGAAGCGTGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 399
OY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGGAGGTCTCTGCTGCGAGTGGGCGGAGTGCAGCCAGACCTTGGCTGCCAGGAGAGATGC 459
OY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCGAGTGC 477

```

RESULT 8
AR370880 1265 bp DNA linear PAT 12-SEP-2003
LOCUS AR370880
DEFINITION Sequence 173 from patent US 6395278.
ACCESSION AR370880
VERSION AR370880.1 GI:34607773
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE

1 (bases 1 to 1265)

AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L. and Yugiu, J.

TITLE

Prostate specific fusion protein compositions

JOURNAL

Patent: US 6395278-A 173 28-MAY-2002;
Corixa Corporation; Seattle, WA
Location/Qualifiers
1..1265
/organism="unknown"

ORIGIN

/mol_type="genomic DNA"

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
9.47e-65	1265	146	0	0	0	0
Score:	758.00					
Percent Similarity:	100.0%					
Best Local Similarity:	100.0%					
Query Match:	100.0%					

US-10-726-093-10 (1-146) x AR370880 (1-1265)

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OY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValIleuSerAla 20
DB 40 ATGGAACAGAAATGTTCTGCTCGGCGCTCGTGCATCCGACATGGAGTGTCTGACGCC 99
OY 21 AlaHisCysPheGlnAsnSerTyrrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCAGAACTCTTACACCTCCTGAGCTGGAGCTGAGCTGAGCTGAGCTGAG 159
OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60
DB 160 CAAAGCCAGGAGGAGCAGATGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 219
OY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGTCTGCTTACACCTCCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 279
OY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGGAGCATGACATGCTTGTGCGAGTGCATCCGCGGAGAACTTTGCCCTC 339
OY 101 ValSerGlyTyrPglYLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTTCGTGCTGGGCTGCTGCGAAGCGTGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 399
OY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGGAGGTCTCTGCTGCGAGTGGGCGGAGTGCAGCCAGACCTTGGCTGCCAGGAGAGATGC 459
OY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCGAGTGC 477

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RESULT 9
AR392385 1265 bp DNA linear PAT 18-DEC-2003
LOCUS AR392385
DEFINITION Sequence 173 from patent US 6613872.
ACCESSION AR392385
VERSION AR392385.1 GI:40116406
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE

1 (bases 1 to 1265)

AUTHORS Xu, J. and Dillon, D.C.

TITLE

Compounds for immunotherapy of prostate cancer and methods for
their use

JOURNAL

Patent: US 6613872-A 173 02-SEP-2003;
Corixa Corporation; Seattle, WA
Location/Qualifiers
1..1265
/organism="unknown"
/mol_type="genomic DNA"

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:
9.47e-65	1265	146	0	0	0
Score:	758.00				
Percent Similarity:	100.0%				
Best Local Similarity:	100.0%				
Query Match:	100.0%				

DB: 2 Gaps: 0

US-10-726-093-10 (1-146) x AR392385 (1-1265)

Qy 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
 |||
 Db 40 ATGGAAGAAAGCAATTGTTCTGCGGCGTCTGTCGATCCGAGTGGCTCTGTACGCC 99
 |||

Qy 21 AlaHisCysPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
 |||
 Db 100 GCACACGTTTCCAGAACTCCTACACCATCGGGCTGGCTGCACAGTCTTGAGCGCGAC 159
 |||

Qy 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyTrpAsn 60
 |||
 Db 160 CAAGAGCCAGAGGAGCCAGATGCTGAGAGCCAGCTCTCCGACGCGACCCAGAGTACAC 219
 |||

Qy 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
 |||
 Db 220 AGACCTTGCTGCTGCTACAGACCTCATGCTCATCAAGTTGACGAATCCGTTCCGAGTCT 279
 |||

Qy 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
 |||
 Db 280 GACCCATCCGAGACATCAGCATGCTTCCGAGTCCCTACCGGGGAATCTTGGCTC 339
 |||

Qy 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
 |||
 Db 340 GTTCTGCGTGGGCTGCTGCTGCGAACGGTACGCTCAAGGCTGTGTCTGCTCTTCA 399
 |||

Qy 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
 |||
 Db 400 AGAGAGTCTCTGCTGCTGCGGAGCGGCTGACCCAGAGCTGTGCTGCCAGAGATGC 459
 |||

Qy 141 LeuProCysCysSerAla 146
 |||
 Db 460 CTACCGTGGCTGCAATGCG 477
 |||

RESULT 10
 AR400020 1265 bp DNA linear PAT 18-DEC-2003
 LOCUS Sequence 173 from patent US 6620922.
 DEFINITION AR400020
 ACCESSION AR400020
 VERSION AR400020.1 GI:40143007
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1265)
 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
 TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
 JOURNAL Patent: US 6620922-A 173 16-SEP-2003;
 Corixa Corporation; Seattle, WA
 FEATURES
 source Location/Qualifiers
 1..1265
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Alignment Scores: Pred. No.: 9.47e-65 Length: 1265
 Score: 758.00 Matches: 146
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-726-093-10 (1-146) x AR400020 (1-1265)

Qy 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
 |||
 Db 40 ATGGAAGAAAGCAATTGTTCTGCGGCGTCTGTCGATCCGAGTGGCTCTGTACGCC 99
 |||

Db 40 ATGGAAGAAAGCAATTGTTCTGCGGCGTCTGTCGATCCGAGTGGCTCTGTACGCC 99
 |||

Qy 21 AlaHisCysPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
 |||
 Db 100 GCACACGTTTCCAGAACTCCTACACCATCGGGCTGGCTGCACAGTCTTGAGCGCGAC 159
 |||

Qy 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyTrpAsn 60
 |||
 Db 160 CAAGAGCCAGAGGAGCCAGATGCTGAGAGCCAGCTCTCCGACGCGACCCAGAGTACAC 219
 |||

Qy 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
 |||
 Db 220 AGACCTTGCTGCTGCTACAGACCTCATGCTCATCAAGTTGACGAATCCGTTCCGAGTCT 279
 |||

Qy 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
 |||
 Db 280 GACCCATCCGAGACATCAGCATGCTTCCGAGTCCCTACCGGGGAATCTTGGCTC 339
 |||

Qy 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
 |||
 Db 340 GTTCTGCGTGGGCTGCTGCTGCGAACGGTACGCTCAAGGCTGTGTCTGCTCTTCA 399
 |||

Qy 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
 |||
 Db 400 AGAGAGTCTCTGCTGCTGCGGAGCGGCTGACCCAGAGCTGTGCTGCCAGAGATGC 459
 |||

Qy 141 LeuProCysCysSerAla 146
 |||
 Db 460 CTACCGTGGCTGCAATGCG 477
 |||

RESULT 11
 AR405287 1265 bp DNA linear PAT 18-DEC-2003
 LOCUS Sequence 173 from patent US 6630305.
 DEFINITION AR405287
 ACCESSION AR405287
 VERSION AR405287.1 GI:40154124
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1265)
 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
 TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
 JOURNAL Patent: US 6630305-A 173 07-OCT-2003;
 Corixa Corporation; Seattle, WA.
 FEATURES
 source Location/Qualifiers
 1..1265
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Alignment Scores: Pred. No.: 9.47e-65 Length: 1265
 Score: 758.00 Matches: 146
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-726-093-10 (1-146) x AR405287 (1-1265)

Qy 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
 |||
 Db 40 ATGGAAGAAAGCAATTGTTCTGCGGCGTCTGTCGATCCGAGTGGCTCTGTACGCC 99
 |||

Qy 21 AlaHisCysPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
 |||
 Db 100 GCACACGTTTCCAGAACTCCTACACCATCGGGCTGGCTGCACAGTCTTGAGCGCGAC 159
 |||

Qy	41	GlnGlnuProGlySerGlnMetValGluAlaSerLeuSerValAlaArgHisProGluuTYrAsn	60
Db	160	CAAGAGCCAGGAGACCAGATGGTGGAGGCCAGCTCTCCGTAAGGACCCAGATAC	219
Qy	61	ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer	80
Db	220	AGACCTTGCTGCTTACGACCTTATGCTCATCAAGTTGAGCAATCGTGTCCGAGTCT	279
Qy	81	AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGluAsnSerCysLeu	100
Db	280	GACACCATCCGAGCATCAGCATGCTTCCGACAGGCCCTACCCGGGGGAACTCTTGCTC	339
Qy	101	ValSerGlyTTPGlyLeuLeuAlaAsnGluValGluLeuThrGlyValCysLeuProSerSer	120
Db	340	GTTTCGTGGCTGGGCTGCTGCTGGCAGCGTGAAGCTCAGCGGTGTGTGTCTCCCTTTCA	399
Qy	121	ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys	140
Db	400	AGGAGTCTCTTGCCCACTGCGGGGGCTGACCCAGAGCTCTCGCTCCAGGCAAGATGC	459
Qy	141	LeuProCysCysSerAla	146
Db	460	CTACCGTGTCTGACATGCGC	477
RESULT 12			
LOCUS	AR439491	1265 bp	DNA
DEFINITION	Sequence 173 from patent US 6664377.		linear
ACCESSION	AR439491		
VERSION	AR439491.1	GI:42665400	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1265)		
TITLE	Xu, J.		
JOURNAL	Compounds for immunotherapy of prostate cancer and methods for their use		
	Patent: US 6664377-A 173 16-DEC-2003;		
	Cortixa Corporation; Seattle, WA;		
	WOX;		
FEATURES			
source	Location/Qualifiers		
	1..1265		
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	/mol_type="genomic DNA"		
ORIGIN			
Alignment Scores:			
Pred. No.:	9, 47e-65	Length:	1265
Score:	758.00	Matches:	146
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
	2	Gaps:	0
Db:			
US-10-726-093-10 (1-146) x AR439491 (1-1265)			
Qy	1	MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla	20
Db	40	ATGGAAAACAAATTGTTCTGCTGGGGCTCTGTGTCATCCGACAGTGGTGTGACGCC	99
Qy	21	AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp	40
Db	100	GCACACTGTTTCCAGAACTCTACACCATCGGGCTGGGCTCGACACACTTGAAGCCGAC	159
Qy	41	GlnGlnuProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluuTYrAsn	60
Db	160	CAAGAGCCAGGAGACCAGATGGTGGAGGCCAGCTCTCCGTAAGGACCCAGATAC	219
Qy	61	ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer	80
Db	220	AGACCTTGCTGCTTACGACCTTATGCTCATCAAGTTGAGCAATCGTGTCCGAGTCT	279

QY	81	AspThrIleArgSerTleSerTleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu	100
Db	280	GAACCATCCGAGCATCAGCATTTGCTTGCGAGTGCCTTACCGCGGAACTCTTGCC	339
QY	101	ValSerGlyTTrGlyIleuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer	120
Db	340	GTTCCTGGCTGGGGTCTGCTGGGAACGGTAGCTCACGGGTGTGTGTCTGGCCCTTCA	399
QY	121	ArgArgSerSerAlaGlnSerAlaArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlyCys	140
Db	400	AGAGGTCTCTCTCCACAGTCCGGGGGGCTGACCCAGAGCTCTGGCTGCCAGGCAAGATGC	459
QY	141	LeuProCysCysSerAla	146
Db	460	CTACCGTGCTGCAGTGGC	477
RESULT 13			
AR563667		1265 bp	DNA
LOCUS			linear
DEFINITION			PAT 08-OCT-2004
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
ORIGIN			
Alignment Scores:			
Pred. No.:			
Score:			
Percent Similarity:			
Best Local Similarity:			
Query Match:			
DB:			
US-10-726-093-10 (1-146) x AR563667 (1-1265)			
QY	1	MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTTrValLeuSerAla	20
Db	40	ATGGAAAGCATTTGTTCTGCTCGGGCGCTGGTGTCAGTCCGACGTGGTGTCTGACGC	99
QY	21	AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerIleuGlnAlaAsp	40
Db	100	GCACACTGTTTCAGAACTCTTACACCAATCCGCGGGCTGGCTGCACACGCTTTAGGCCGAC	159
QY	41	GlnGluProGlySerGlnMetValGlnAlaSerLeuSerValArgHisProGluTyrAsn	60
Db	160	CAGAGCCAGGAGCCAGATGTGTGAGGCCACCTCTCCGTACGGCACCCAGATGATCAAC	219
QY	61	ArgProLeuLeuAlaAsnAspLeuMetIleuIleCysLeuAspGluSerValSerGluSer	80
Db	220	AGACCTTCTGCTGCTAACGACCTCATGCTCATCAAGTTGAGCAATCCGTGTCGAGTCT	279
QY	81	AspThrIleArgSerTleSerTleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu	100
Db	280	GAACCATCCGAGCATCAGCATTTGCTTGCGAGTGCCTTACCGCGGAACTCTTGCC	339
QY	101	ValSerGlyTTrGlyIleuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer	120

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Db      340 GTTCTGCTGGGGCTGCTGGCGAAGCTGAGCTCAGGCTGTGTCTGCCCTCTTCA 399
QY      121 ATGATGSerSerAlaGlnSerArgGlyLeuThGlnSerSerAlaGlnGluCys 140
Db      400 AGGAGGCTCTGCTGCGGAGCGGGGCTGACCCAGAGCTCTGCTGCCAGGAGAAATGC 459
QY      141 LeuProCysCysSerAla 146
Db      460 CTACCGTGCTGCAGTGGC 477

RESULT 14
LOCUS   AR588653 1265 bp DNA linear PAT 15-DEC-2004
DEFINITION
Sequence 173 from patent US 6800746.
ACCESSION AR588653
VERSION   AR588653.1 GI:56635550
KEYWORDS
SOURCE   Unknown.
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 1265)
AUTHORS  Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
          Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
          Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
          Hepler,W.T. and Henderson,R.A.
          Compositions and methods for the therapy and diagnosis of prostate
          cancer
JOURNAL Patent: US 6800746-A 173 05-OCT-2004;
FEATURES
source Corixa Corporation; Seattle, WA
location/Qualifiers
1..1265
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 9,47e-65 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-726-093-10 (1-146) x AR588653 (1-1265)
QY      1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
Db      40 ATGGAAGAACGAAATTGTTCTGCTGGGGCTGCTGTCATCCGAGTGGGTGCTGACGC 99
QY      21 AlaHisCysPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
Db      100 GCACACTGTTTCCAGAACTCTTACACCATCGGGCTGGGCTGCACAGTCTTGAAGCCGAC 159
QY      41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60
Db      160 CAAGAGCCAGGAGCCGAGATGGTGGAGCCAGCTTCCCTACCGCACCCAGAGTCAAC 219
QY      61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGlnSerValSerGlnUser 80
Db      220 AGACCTTGTCTGCTAAGCACTTATCTCATCAAGTTGAGCAATCCGTCCGAGTCT 279
QY      81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
Db      280 GACACCATCCGAGCATCAGCATGCTTCCAGAGCCCTACCCGCGGGAATCTTGCCTC 339
QY      101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
Db      340 GTTTCCTGGGTGGGTCTGGTGGAGAGGTGAGTCAAGGGGTGTGTCTGCTCTTCA 399
QY      121 ArgArgSerSerAlaGlnSerArgGlyLeuThGlnSerSerAlaSerGlnAlaGluCys 140
Db      400 AGGAGGCTCTGCTGCGGAGTGGCGGGGCTGACCCAGAGCTCTGCTGCCAGGAAATGC 459

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QY      141 LeuProCysCysSerAla 146
Db      460 CTACCGTGCTGCAGTGGC 477

RESULT 15
LOCUS   AR605473 1265 bp DNA linear PAT 15-DEC-2004
DEFINITION
Sequence 173 from patent US 6818751.
ACCESSION AR605473
VERSION   AR605473.1 GI:56657137
KEYWORDS
SOURCE   Unknown.
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 1265)
AUTHORS  Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
          Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
          Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
          Hepler,W.T. and Henderson,R.A.
          Compositions and methods for the therapy and diagnosis of prostate
          cancer
JOURNAL Patent: US 6818751-A 173 16-NOV-2004;
FEATURES
source Corixa Corporation; Seattle, WA
location/Qualifiers
1..1265
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 9,47e-65 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-726-093-10 (1-146) x AR605473 (1-1265)
QY      1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
Db      40 ATGGAAGAACGAAATTGTTCTGCTGGGGCTGCTGTCATCCGAGTGGGTGCTGACGC 99
QY      21 AlaHisCysPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
Db      100 GCACACTGTTTCCAGAACTCTTACACCATCGGGCTGGGCTGCACAGTCTTGAAGCCGAC 159
QY      41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60
Db      160 CAAGAGCCAGGAGCCAGATGGTGGAGCCAGCTTCCCTACCGCACCCAGAGTCAAC 219
QY      61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGlnSerValSerGlnUser 80
Db      220 AGACCTTGTCTGCTAAGCACTTATCTCATCAAGTTGAGCAATCCGTCCGAGTCT 279
QY      81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
Db      280 GACACCATCCGAGCATCAGCATGCTTCCAGAGCCCTACCCGCGGGAATCTTGCCTC 339
QY      101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
Db      340 GTTTCCTGGGTGGGTCTGGTGGAGAGGTGAGTCAAGGGGTGTGTCTGCTCTTCA 399
QY      121 ArgArgSerSerAlaGlnSerArgGlyLeuThGlnSerSerAlaSerGlnAlaGluCys 140
Db      400 AGGAGGCTCTGCTGCGGAGTGGCGGGGCTGACCCAGAGCTCTGCTGCCAGGAAATGC 459

```

Thu Aug 31 12:47:23 2006

us-10-726-093-10.rge

Page 9

Search completed: August 28, 2006, 19:37:59
Job time : 3300 secs

GenCore version 5.1.9
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OW protein - nucleic search, using frame_plus_p2n model

Run on: August 28, 2006, 18:09:15 ; Search time 521 Seconds
(without alignments)
2930.753 Million cell updates/sec

Title: US-10-726-093-10
Perfect score: 758
Sequence: 1 MENELFCGVLVHPQWLSA.....SRGLTSSASQAECIPCCSA 146

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5244920 seqs, 3486124231 residues
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/abse/ABSSWB.spool/US10726093/runat_28082006.121133_25490/app.query.fasta_1
-DB=N.Geneseq -OFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs03p
-USER=US10726093 @CGN 1.1.1147 @runat_28082006.121133_25490 -NCPU=6 -ICPU=3
-NO MMAP -NCG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N.Geneseq.8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
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13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	758	100.0	702	4	AAC90119 Human pro
2	758	100.0	848	8	ABQ83341 Human KLK
3	758	100.0	1265	2	AAV58645 Prostate

4	758	100.0	1265	2	AAV61250 CDNA sequ
5	758	100.0	1265	3	AA06408 Human imm
6	758	100.0	1265	3	ABE71313 Human pro
7	758	100.0	1265	4	AAH93524 Human pro
8	758	100.0	1265	4	AAH93524 Human pro
9	758	100.0	1265	4	AAH93524 Human pro
10	758	100.0	1265	4	AAH84838 Human pro
11	758	100.0	1265	5	ACA59425 Prostate
12	758	100.0	1265	5	AAH84838 Human pro
13	758	100.0	1265	6	ABH94988 Human pro
14	758	100.0	1265	6	ABH94988 Human pro
15	758	100.0	1265	6	ABH94988 Human pro
16	758	100.0	1265	10	ADG26039 Human pro
17	758	100.0	1265	10	ADG26039 Human pro
18	758	100.0	1265	15	AEF66320 Human pro
19	758	100.0	1265	15	AEF66320 Human pro
20	660	87.1	4385	8	ABQ83347 Human KLK
21	660	87.1	4740	3	AAV58646 Prostate
22	660	84.4	1459	2	AAV58646 Prostate
23	660	84.4	1459	2	AAV61251 CDNA sequ
24	660	84.4	1459	3	AAV61251 CDNA sequ
25	660	84.4	1459	3	AAV61251 CDNA sequ
26	660	84.4	1459	4	AAH93525 Human pro
27	660	84.4	1459	4	AAH93525 Human pro
28	660	84.4	1459	4	AAH93525 Human pro
29	660	84.4	1459	5	ACA59426 Prostate
30	660	84.4	1459	5	ACA59426 Prostate
31	660	84.4	1459	5	AAH84839 Human pro
32	660	84.4	1459	6	AAH84839 Human pro
33	660	84.4	1459	6	AAH84839 Human pro
34	660	84.4	1459	10	ADH13624 Human pro
35	660	84.4	1459	10	ADH13624 Human pro
36	660	84.4	1459	10	ADG26040 Human pro
37	660	84.4	1459	15	AEF66321 Human pro
38	660	84.4	1459	15	AEF66321 Human pro
39	612	80.7	834	4	AAH93525 Human pro
40	588	77.6	618	4	AAH93525 Human pro
41	588	77.6	618	4	AAH93525 Human pro
42	588	77.6	748	4	AAH93525 Human pro
43	588	77.6	765	4	AAH93525 Human pro
44	588	77.6	765	4	AAH93525 Human pro
45	588	77.6	765	4	AAH85135 Human pro

ALIGNMENTS

RESULT 1	AAC90119	standard; CDNA; 702 BP.
ID	AAC90119	
XX	AAC90119	
AC	AAC90119	
XX	AAC90119	
DT	14-MAR-2001 (first entry)	
DE	Human prostate cancer-related intracellular protein CDNA #3.	
XX	Human; prostate cancer; intracellular protein; cytosolic; gene therapy;	
KW	breast cancer; ss.	
XX	Homo sapiens.	
OS	Homo sapiens.	
PN	WO200071711-A2.	
XX	30-NOV-2000.	
PD	30-NOV-2000.	
XX	19-MAY-2000; 2000WO-IB000673.	
PF	19-MAY-2000; 2000WO-IB000673.	
XX	20-MAY-1999; 99US-0135325P.	
PR	20-MAY-1999; 99US-0135333P.	
XX	(SAAT/) SAATCIOGLU F.	
PA	(SAAT/) SAATCIOGLU F.	
XX	SAATCIOGLU F;	
PI	SAATCIOGLU F;	

XX MPI; 2001-032036/04.
DR P-PSDB; AAB50449.
XX
XX Novel nucleic acids encoding intracellular proteins useful for detecting
PT neoplastic cell in a mammal, preferably the presence of prostate cancer
PT or breast cancer.
XX
PS Claim 5; Page 17-18; 47pp; English.
XX
XX The present sequence encodes an intracellular protein which is
CC differentially expressed in neoplastic cells, particularly prostate
CC cancer cells. The polynucleotides and polypeptides are useful for
CC diagnosing or detecting prostate cancer and breast cancer cells. The
CC polynucleotides and polypeptides are also useful for treating cancer by
CC antisense therapy and antibody based therapy, respectively.
XX
SQ Sequence 702 BP; 135 A; 207 C; 213 G; 147 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 3,71e-70 Length: 702
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0
US-10-726-093-10 (1-146) x AAC90119 (1-702)
QY 1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
Db 1 ATGGAAGAAAGCAATGTTCTGCTGGCGGCGTCTCGTGGCAATCCGACATGGGTGCTGCACACC 60
QY 21 AlaHisCysPheGlnAsnSerTyrrHisLeuGlyLeuHisSerLeuGluAlaAsp 40
Db 61 GCACACTGTTTCCAAACTCTCTACACCACTCGGGCTGGGCTGCACAGCTTGAGGCCGAC 120
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpAsn 60
Db 121 CAAGAGCCAGGGAGCCAGATGGTGGAGGCCACCTCTCCGTAAGGCCACCAAGATCAAC 180
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
Db 181 AGACCTTGTCTCGCTACAGACTCTCTCATCAAGATTGAGAGAACTCGTGTCCAGTCT 240
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
Db 241 GACACCAATCCGAGCATCAAGATGCTCTGCGAGTCCCTTACCGCGGGAACTCTTGCCCTC 300
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyLeuThrGlyValCysLeuProSerSer 120
Db 301 GTTCTGGCTGGGCGTCTGCTGGCGAAGCGTGAAGCTCAGGGGTGTGTCTGCTGCTTCA 360
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
Db 361 AGGAGGTCTCTGCCAGTCCGCGGGGCTGACCCAGCAAGCTTGCCTCCAGGACAGAAATGC 420
QY 141 LeuProCysCysSerAla 146
Db 421 CTACCGTCTCTGAGTCCG 438
RESULT 2
ID ABO83341 standard; cDNA; 848 BP.
XX ABO83341;
XX
XX 20-JAN-2003 (first entry)
XX
XX Human KLK4 alternatively spliced variant encoding cDNA SEQ ID NO:1.
XX
XX Human; KLK4; cancer; benign tumour; cytostatic; variant; gene; ss.
XX

OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1.588
FT CDS /*tag= a
FT /product= "KLK4 alternatively spliced variant"
XX
XX W0200277243-A1.
XX
XX 03-OCT-2002.
XX
XX 27-MAR-2002; 2002WO-AU000378.
XX
XX 27-MAR-2001; 2001AU-00004022.
XX
XX (U90U-) UNIV QUEENSLAND TECHNOLOGY.
XX
XX Dong Y, Clements JA;
XX
XX MPI; 2003-029939/02.
DR P-PSDB; ABP54355.
XX
XX Detecting the presence or diagnosing the risk of cancer or benign tumor,
PT e.g. an ovarian, endometrial or prostate cancer, by determining the
PT presence of or detecting aberrant expression of KLK4 in a biological
PT sample from the patient.
XX
XX Claim 59; Page 106-107; 126pp; English.
XX
XX The present invention describes a method (M1) for detecting the presence
CC or diagnosing the risk of cancer or benign tumor in a patient. M1
CC comprises determining the presence of or detecting aberrant expression of
CC KLK4 in a biological sample obtained from the patient. KLK4 has
CC cytosolic activity. The method is useful for detecting the presence or
CC diagnosing the risk of a cancer or a benign tumor in a patient,
CC particularly an ovarian, endometrial or prostate cancer, or a cancer or
CC benign tumor associated with an organ or tissue from the ovaries,
CC endometrium or prostate. An agent which can be used for restoring or
CC modulating KLK4 expression can be used for treating or preventing cancer
CC or benign tumor. KLK4 polynucleotides, polypeptides or antigen-binding
CC molecules from the present invention can be used for detecting aberrant
CC KLK4 polynucleotides or aberrant K4 polypeptides that correlate with a
CC cancer or a benign tumor. The present sequence encodes a human KLK4
CC alternatively spliced variant from the present invention.
XX
SQ Sequence 848 BP; 162 A; 254 C; 257 G; 175 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4.8e-70 Length: 848
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0
US-10-726-093-10 (1-146) x ABO83341 (1-848)
QY 1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
Db 148 ATGGAAGAAAGCAATGTTCTGCTGGCGGCGTCTCGTGGCAATCCGACATGGGTGCTGCACACC 207
QY 21 AlaHisCysPheGlnAsnSerTyrrHisLeuGlyLeuHisSerLeuGluAlaAsp 40
Db 208 GCACACTGTTTCCAAACTCTCTACACCACTCGGGCTGGGCTGCACAGCTTGAGGCCGAC 267
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpAsn 60
Db 268 CAAGAGCCAGGGAGCCAGATGGTGGAGGCCACCTCTCCGTAAGGCCACCAAGATCAAC 327
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
Db 328 AGACCTTGTCTCGCTACAGACTCTCATCAAGATTGAGAGAACTCGTGTCCAGTCT 387

Qy	81	AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaIleValAsnSerCysLeu	109
Db	388	GACACCATCCGGAGCATCAGCATTCCTTCGCGAGTCCCTACCGCGGGAACTCTTGCTC	447
Qy	101	ValSerGlyThrGlyIleuLeuAlaAsnGlyIleuThrGlyValCysLeuProSerSer	120
Db	448	GTTTCGGCTGGGGGTGCTGGCGAAGGTAGCTCAGGGGTGTGTCTGCCCTTTCA	507
Qy	121	ArgArgSerSerAlaIleuSerArgGlyIleuThrGlnSerSerAlaSerGlnAlaGluCys	140
Db	508	AGGAGGTCTCTGTCCCAAGTCGGCGGGGCTGACCCAGAGCTGTGCTCCACAGCAGAAATGC	567
Qy	141	LeuProCysCysSerAla 146	
Db	568	CTACCGTGTGTCAGTGC 585	
RESULT 3			
ID	AAV58645	standard; cDNA; 1265 BP.	
XX	AAV58645;		
XX	AAV58645;		
DT	25-MAR-2003	(revised)	
DT	08-DEC-1998	(first entry)	
XX	Prostate tumour specific gene clone D62.		
DE	Prostate tumour specific gene; human; prostate cancer; detection;		
KW	therapy; ss.		
XX	Homo sapiens.		
OS	W09837418-A2.		
XX	27-AUG-1998.		
PD	25-FEB-1998;	98WO-US003690.	
PF	25-FEB-1997;	97US-008064596.	
XX	01-AUG-1997;	97US-00804809.	
PR	09-FEB-1998;	98US-00020747.	
PA	(CORI-) CORIXA CORP.		
XX	Xu J, Dillon DC;		
PI	WPI; 1998-480805/41.		
XX	Novel human prostate specific tumour protein and fragments - useful for		
PT	detecting and treating prostate cancers.		
XX	Claim 1; Page 113-114; 141pp; English.		
PS	This sequence represents a human prostate tumour specific gene, and can		
XX	be used in the method of the invention. The method is for detecting		
CC	prostate cancer comprises contacting a biological sample with an agent		
CC	able to bind an immunogenic portion of a prostate protein (such as		
CC	encoded by this sequence). An antibody which binds to an immunogenic		
CC	portion of the prostate protein, and the method can be used to detect,		
CC	monitor progression of, or treat prostate cancers. The antibody may also		
CC	be conjugated to a therapeutic agent for use in therapy of prostate		
CC	cancers. (Updated on 25-MAR-2003 to correct PR field.)		
XX			
SO	Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;		
Alignment Scores:			
Pred. No.:	8,296-70	Length:	1265
Score:	758.00	Matches:	146
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-726-093-10 (1-146) x AAV58645 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTPValLeuSerAla 20
Db 40 ATGGAAAAACAATGTCTCTGCTCGGGCGCTCTGGTGCATCCGAGTGGGTCTGTCAACC 99
QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
Db 100 GCACACAGTGTTCAGAACTCTTACACCATCGGGCTGGGCTTCACACAGTCTTGAAGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValAlaArgHisProGluTyrAsn 60
Db 160 CAAAGCCAGGAGACCCAGATGATGGAGCCAGCTTCGGTACCGGACCCAGACTACAAAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80
Db 220 AGACCTCTGCTCGCTACAGACCTCATCTCATCAAGTTGAGCGAATCCGTGTCCGAGTCT 279
QY 81 AspThrIleAsnSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
Db 280 GACACCAATCCGAGCATCAGCATTCCTTCGACAGCCCTACCGGGGGAACTTTGGCTTC 339
QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
Db 340 GTTTCGTGGCTGGGTCTGCTGGCGAAGCGTAGCTCAAGGGTGTGTCTGCTCCCTTTC 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
Db 400 AGGAGGTCTCTGCGCCAGTCCGCGGGGGCTGACCCAGAGCTCTGCTGCCAGCAAGATGC 459
QY 141 LeuProCysCysSerAla 146
Db 460 CTACCGTGTCTCAAGTGC 477

RESULT 4
AAV61250
ID AAV61250 standard: cDNA, 1265 BP.
AC AAV61250;
XX
DT 06-JAN-1999 (first entry)
XX
DE cDNA sequence of prostate tumour clone P703 splice variant DE2.
XX
KM Prostate; cancer; tumour; vaccine; immunogen; clone; ss.
XX
OS Homo sapiens.
XX
PN WO9837093-A2.
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO-US003492.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC;
XX
DR WPI; 1998-609886/51.
XX
PT Polypeptides comprising immunogenic portions of prostate proteins - used
PS in a vaccine for the treatment of prostate cancer.
XX
PS Claim 3; Page 105-106; 130pp; English.
XX
CC The present sequence is a new DNA which encodes an immunogenic portion of
CC a prostate tumour protein. The encoded immunogen, or the DNA itself, can
CC be used as a vaccine for the treatment of prostate cancer. The DNA was
CC identified by analysis of a substracted cDNA library obtained by

CC subtracting a prostate tumour cDNA expression library with a normal
CC tissue cDNA library
XX
SQ Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;

Alignment Scores:

Pred. No.:	8.29e-70	Length:	1265
Score:	758.00	Matches:	146
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-726-093-10 (1-146) x AAV61250 (1-1265)

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QY      1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTPValLeuSerAla 20
DB      40 ATGGAAAACGAATTGTTCTGCTCGGGGCTCTGTGTCATCCGAGTGGGTCTTCAGCC 99
QY      21 AlaHisCysPheGlnAnsSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB      100 GCACACTGTTTCCAGAACTCTTACACCATCGGGCTGGCTGCACACTTTGAGGCCGAC 159
QY      41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyraSn 60
DB      160 CAAAGAGCCAGGAGCCAGATGTGTGGAGCCAGCTCTCCCTACGGCACCCAGAGTACAC 219
QY      61 ArgProLeuLeuAlaAnsApLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB      220 AGACCTTGCTGCTTAACGACCTCATCTCATCAAGTTGAGACGAATCCGTCGAGTCT 279
QY      81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAnsSerCysLeu 100
DB      280 GACACCATCCGAGCATCAGCATGCTTCGACAGGCCCTACCGGGGGAACCTTGGCTC 339
QY      101 ValSerGlyTTPGlyLeuLeuAlaAnsGlyGlyLeuThrGlyValCysLeuProSerSer 120
DB      340 GTTCTGGCTGGGGTGTGTGGCGAAGGTGAGCTCAGGGGTGTGTGCTTCCCTTTCA 399
QY      121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB      400 AGAGAGTCTCTGCTCCCACTGCGGGGGGCTGACCCAGAGCTCTGGTCCCAAGCAATGC 459
QY      141 LeuProCysCysSerAla 146
DB      460 CTACCGTGTGACGTGCG 477

```

RESULT 5

AAA06408
ID AAA06408 standard; cDNA; 1265 BP.

AC AAA06408;

XX
XX 13-JUN-2000 (first entry)

DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:173.

KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cyrostatic; vaccine; se.

OS Homo sapiens.

XX
XX WO200004149-A2.

XX
XX 27-JAN-2000.

XX
XX 14-JUL-1999; 99MO-US015838.

XX
XX 14-JUL-1998; 98US-00115453.

XX
XX 14-JUL-1998; 98US-00116134.

XX
XX 23-SEP-1998; 98US-00159812.

XX
XX 23-SEP-1998; 98US-00159822.

XX
XX 15-JAN-1999; 99US-00232149.

PR 15-JAN-1999; 99US-00232880.
PR 09-APR-1999; 99US-00288946.
XX
XX
XX (CORI-) CORIXA CORP.

PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;

DR WPI; 2000-171268/15.

PT New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein.

XX Claim 1; Page 157; 263pp; English.

XX The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumor protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express the
CC polypeptides, antibodies against the polypeptides and vaccines comprising
CC them can be used for inhibiting the development of prostate cancer in a
CC patient. The polypeptides can be used to generate antibodies or anti-
CC idioypic antibodies for passive immuno therapy. A portion of the
CC polynucleotides encoding the polypeptides can be used as a probe or to
CC modulate the expression of the polypeptides. AA06241 to AA06691 and
CC AAY82000 to AAY82020 represent sequences used in the exemplification of
CC the present invention

SQ Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;

Alignment Scores:

Pred. No.:	8.29e-70	Length:	1265
Score:	758.00	Matches:	146
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-726-093-10 (1-146) x AAA06408 (1-1265)

```

QY      1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTPValLeuSerAla 20
DB      40 ATGGAAAACGAATTGTTCTGCTCGGGGCTCTGTGTCATCCGAGTGGGTCTTCAGCC 99
QY      21 AlaHisCysPheGlnAnsSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB      100 GCACACTGTTTCCAGAACTCTTACACCATCGGGCTGGCTGCACACTTTGAGGCCGAC 159
QY      41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyraSn 60
DB      160 CAAAGAGCCAGGAGCCAGATGTGTGGAGCCAGCTCTCCGTACGGGACCCAGAGTACAC 219
QY      61 ArgProLeuLeuAlaAnsApLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB      220 AGACCTTGCTGCTTAACGACCTCATCTCATCAAGTTGAGACGAATCCGTCGAGTCT 279
QY      81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAnsSerCysLeu 100
DB      280 GACACCATCCGAGCATCAGCATGCTTCGACAGGCCCTACCGGGGGAACCTTGGCTC 339
QY      101 ValSerGlyTTPGlyLeuLeuAlaAnsGlyGlyLeuThrGlyValCysLeuProSerSer 120
DB      340 GTTCTGGCTGGGGTGTGTGGCGAAGGTGAGCTCAGGGGTGTGTGCTTCCCTTTCA 399
QY      121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB      400 AGAGAGTCTCTGCTCCCACTGCGGGGGGCTGACCCAGAGCTCTGGTCCCAAGCAATGC 459
QY      141 LeuProCysCysSerAla 146
DB      460 CTACCGTGTGACGTGCG 477

```

RESULT 6

AB571313
ID AB571313 standard; cDNA; 1265 BP.
XX
AC AB571313;
XX
DT 27-NOV-2002 (first entry)
XX
DE Human prostate tumour protein partial DNA sequence #163.
XX
KW Human; immunogenic; prostate protein; prostate tumour protein;
XX
KW prostate cancer; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN US2002090372-A1.
XX
PD 11-JUL-2002.
XX
PF 14-JUL-1998; 98US-00115453.
XX
PR 25-FEB-1997; 97US-00806099.
XX
PR 01-AUG-1997; 97US-00904804.
XX
PR 09-FEB-1998; 98US-00020956.
XX
PR 25-FEB-1998; 98US-00030607.
XX
PA (XUJ/) XU J.
XX
PA (DILL/) DILLON D C.
XX
PI Xu J, Dillon DC;
XX
DR WPI; 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer
XX
PT comprises an immunogenic portion of prostate tumor protein.
XX
PS Claim 3; Page 78-79; 101pp; English.
XX
CC The present invention relates to a new polypeptide comprising an
XX
CC immunogenic portion of a prostate protein. The invention is useful for
XX
CC inhibiting the development of prostate cancer in a patient. The invention
XX
CC is also useful as markers for diagnosing prostate cancer and for
XX
CC monitoring diseases progression in patients. The present nucleic acid
XX
CC sequence represents a DNA sequence that is part of a gene encoding a
XX
CC human prostate tumour protein
XX
SQ Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;
Alignment Scores:
Pred. No.: 8.29e-70 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-726-093-10 (1-146) x AB571313 (1-1265)
QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAGAACAAATTGTTCTCTCGGGGCTCTGTCGATCCGACAGTGGGCTGTCAGCC 99
QY 21 ALAHISCySPheGlnAsnSerTYrThrILegLYLeuGILyLeuHISserLeuGluAlaASP 40
DB 100 GCACACTGTTTCCAGAACTCTACACCATCGGGCTGGGCTTGACAGTCTTGAGGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHISProGlnIUTyrAsn 60
DB 160 CAAGAGCCAGGAGCCAGATGTTGAGGCCAGGCTCTCCGACGGACCCAGAGTACAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuILeysLeuAspGluSerValISerGluSer 80
DB 220 AGACCTTGCTCGTTAAAGACCTCATGCTCATCAAGTTGACGAAATCGGTCCGAGTCT 279

QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGGAGCATCCAGCAATTGCTTCCAGAGCCCTACCGGGGAACTTGCCTC 339
QY 101 ValSerGlyTTPGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGCTGGGGGTCTGCTGCGACGATGAGCTCACGGGTGTGTCTGCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlyCys 140
DB 400 AGGAGGTCTCTTCCCGCAGTGGGGGGCTGACCCAGAGCTTGTGCTCCAGGCAATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCTCACTGCG 477
RESULT 7
AAH93524
ID AAH93524 standard; cDNA; 1265 BP.
XX
AC AAH93524;
XX
DT 04-OCT-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence P703P-DE2.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
XX
KW cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US001574.
XX
PR 14-JAN-2000; 2000US-00483672.
XX
PA (CORI-) CORIAX CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,
XX
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
XX
PI Wang A, Meagher MJ;
XX
DR WPI; 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for diagnosing,
XX
PT monitoring and treating prostate cancer in a patient and for use in
XX
PT vaccines.
XX
PS Claim 1; Page 285-286; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
XX
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
XX
CC and can be used in vaccine production and gene therapy. (I), (II),
XX
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
XX
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and
XX
CC the antibodies are also used in the detection of cancer in a patient. The
XX
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
XX
CC and (II) can be used in vaccines. The antibodies or (I) and (II) can also
XX
CC monitoring the progression of cancer in a patient. (I) and (II) can also
XX
CC be used to improve diagnostic and therapeutic methods for prostate
XX
CC cancer. They can indicate the level of metastasis as well as the prostate
XX
CC volume. AAH93524 to AAH93944 and AAH01115 to AAH01318 represent
XX
CC polynucleotide and amino acid sequences used in the exemplification of
XX
CC the present invention
XX
SQ Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;
Alignment Scores:
Pred. No.: 8.29e-70 Length: 1265
Score: 758.00 Matches: 146

Percent Similarity: 100.0%
 Best Local Similarity: 100.0%
 Query Match: 100.0%
 Gaps: 4
 Conservative: 0
 Mismatches: 0
 Indels: 0

US-10-726-093-10 (1-146) x AAH93524 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
 DB 40 ATGGAAAACGAATTTCTGCTCGGGCGTCTCGGTGCATCCGAGTGGGTCTGCAACC 99
 QY 21 AlaHisCysPheGlnAsnSerTrpThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
 DB 100 GCACACTCTTTCCAGAACTCTTACACCATCCGGCTGGCGCTGCACAGCTTGAGGCCGAC 159
 QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpAsn 60
 DB 160 CAAGAGCCAGGAGGACCAATGTTGGAGGCCAGCTCTCTCGTACGGACCCAGAGTACAC 219
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleGlyLeuAspGluSerValSerGluSer 80
 DB 220 AGACCTTGTCTGCTTACGACCTCATGCTCATCAAGTTGACGAATCCGTGCGAGTCT 279
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
 DB 280 GACACCATCCGAGCATGAGCATGCTTCTGCGAGTCCCTACCGCGGGAACCTTGTGCTC 339
 QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
 DB 340 GTTCTGTGCTGGGCTCTGCTGCGCAACGGTACGCTCAGGGTGTGTCTGCTCTTCA 399
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
 DB 400 AGGAGGTCTCTGCGCCAGTGGCGGGGCTGACCCAGAGCTCTGCTCCAGGACGAATGC 459
 QY 141 LeuProCysCysSerAla 146
 DB 460 CTACCGTGTGCAATGCG 477

RESULT 8

ID AAS63616 standard; cDNA; 1265 BP.

XX AAS63616;

XX AC 29-JAN-2002 (first entry)

XX DT Human prostate cDNA sequence #168.

XX DE Human; prostate cancer; ss; cytosstatic; immunostimulant; tumour.

XX KW Homo sapiens.

XX OS WO200173032-A2.

XX PD 04-OCT-2001.

XX PF 27-MAR-2001; 2001WO-US009919.

XX PR 27-MAR-2000; 2000US-00516857.

XX PR 09-MAY-2000; 2000US-00568100.

XX PR 12-MAY-2000; 2000US-00570737.

XX PR 13-JUN-2000; 2000US-00593793.

XX PR 27-JUN-2000; 2000US-00605783.

XX PR 09-AUG-2000; 2000US-00636215.

XX PR 29-AUG-2000; 2000US-00651236.

XX PR 06-SEP-2000; 2000US-00657279.

XX PR 02-OCT-2000; 2000US-00679426.

XX PR 10-OCT-2000; 2000US-00685166.

XX PR 09-NOV-2000; 2000US-00709729.

XX PA (CORI-) CORIXA CORP.

XX XX

PI Xu J, Dillon DC, Mitcham UL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;
 XX WPI; 2001-639232/73.

PT New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer.

PS Claim 1; Page 287; 579pp; English.

XX The invention relates to isolated prostate-specific polynucleotides,
 CC polypeptides, fusion proteins of the polypeptides, antibodies raised
 CC against the polypeptides (or antigenic epitopes derived from them) and
 CC antigen-presenting cells expressing the polypeptides. The antibodies are
 CC useful for detecting the presence of cancer, especially prostate cancer.
 CC The polypeptides, polynucleotides and the antigen-presenting cells are
 CC useful for stimulating and/or expanding T cells specific for a tumour
 CC protein, and for inhibiting the development of cancer especially prostate
 CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
 CC useful for stimulating an immune response, and for treating cancer. The
 CC oligonucleotide is useful for detecting cancer. The present sequence is a
 CC prostate specific polynucleotide of the invention

XX Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;

XX Alignment Scores:

Pred. No.: 8,29e-70 Length: 1265
 Score: 758.00 Matches: 146
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 4 Gaps: 0

US-10-726-093-10 (1-146) x AAS63616 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20

DB 40 ATGGAAAACGAATTTCTGCTCGGGCGTCTCGGTGCATCCGAGTGGGTCTGCAACC 99

QY 21 AlaHisCysPheGlnAsnSerTrpThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40

DB 100 GCACACTCTTTCCAGAACTCTTACACCATCGGGTGGGCTGACACAGCTTGAAGCCGAC 159

QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpAsn 60

DB 160 CAAGAGCCAGGAGGCCAGATGTTGGAGGCCAGCTCTCCGTACGGACCCAGAGTACAC 219

QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleGlyLeuAspGluSerValSerGluSer 80

DB 220 AGACCTTGTCTGCTTACGACCTCATGCTCATCAAGTTGACGAATCCGTGCGAGTCT 279

QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100

DB 280 GACACCATCCGAGCATGAGCATGCTTCCAGAGCCCTACCGGGGAACCTTGTGCTC 339

QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120

DB 340 GTTCTGTGCTGGGCTCTGCTGCGCAACGGTACGCTCAGGGTGTGTCTGCTCTTCA 399

QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140

DB 400 AGGAGGTCTCTGCGCCAGTGGCGGGGCTGACCCAGAGCTCTGCTCCAGGACGAATGC 459

QY 141 LeuProCysCysSerAla 146

DB 460 CTACCGTGTGCAATGCG 477

RESULT 9

ID AAH02589 standard; cDNA; 1265 BP.

XX AAH02589;

XX AC


```

DB: 4 Gaps: 0
US-10-726-093-10 (1-146) x AAH84838 (1-1265)
QY 1 MetGluAaNGluLeuPheCysSerGlyValLeuValHisProGlnTTPValLeuSerAla 20
DB 40 ATGGAAACGAATTGTTCTGCTCGGCGCTGCTGGTGCATCCGCAATGGGTGCTGCACCC 99
QY 21 AlaHisCysPheGlnAaSerSerThrIleGlyLeuGlyLeuHisSerLeuGluAaSP 40
DB 100 GCACACTGTTTCCAAATCCTTCAACCATCGGCGCTGGGCTGCACAGTCTTAGGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAaSerLeuSerValArgHisProGlnTyrAsn 60
DB 160 CAAGAGCCAGGAGCCAGATGCTGAGAGCCAGCCCTCTCCGTACGGCACCCAGAGTACAAC 219
QY 61 ArgProLeuLeuAlaAaAspLeuMetLeuIleLysLeuAaSPGluSerValSerGluSer 80
DB 220 AGACCTTGTGCTGCTAACGACCTCATGCTCATCAAGTTGAGCAATCCGTGTCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAaSerGlnCysProThrAlaGlyAaSerCysLeu 100
DB 280 GACACCATCCGAGACATACGATTCCTTCTGCAATGCCCGGGGAACTTGGCTTC 339
QY 101 ValSerGlyTTPGlyLeuLeuAlaAaNGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGCTGGGCTGCTGCTGCTGCGAAACGCTGAGCTCAGCGGTGTGTCTGCTCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGGAGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 477
QY
DB
RESULT 11
ID ACAS9425
ID ACAS9425 standard; cDNA; 1265 BP.
AC ACAS9425;
AC
DT 10-JUN-2003 (first entry)
XX
DE Prostate cancer therapy associated cDNA #168.
XX
KM Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KM immunogen; cancer; prostate specific antigen; PSA;
KM prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KM PSMA; gene; ss.
XX
OS Homo sapiens.
XX
XX US2002192763-A1.
PN
XX
PD 19-DEC-2002.
XX
PF 29-JUN-2001; 2001US-00895793.
XX
PR 04-OCT-1999; 99US-0157455P.
PR 04-OCT-2000; 2000US-00679272.
PR 28-MAR-2001; 2001US-00822827.
XX
XX (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARU/) HARLOCKER S L.
PA (JIANG/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) BETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.

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PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUH/) HOUGHTON R L.
PA (DAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D,
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J,
PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;
XX
XX WPI; 2001-245062/25.
DR
XX
XX Prostate specific protein and its encoding polynucleotide, useful for the
XX treatment and diagnosis of prostate cancer.
XX
XX Example 3; SEQ ID NO 173; 85pp; English.
XX
XX The invention describes a fusion protein comprising at least one amino
XX acid sequence of immunogenic portions of any of the 3 sequences: not
XX defined in the specification, or sequences having at least 70 or 90 %
XX sequence identity to any one of the 35 sequences defined in the USPTO web
XX site, which is encoded by any of the 4 nucleotide sequences not defined
XX in the specification. The fusion protein, composition and methods are
XX useful for diagnosing, preventing and/or treating cancer, particularly
XX prostate cancer. The proteins are useful as markers to indicate the
XX presence or absence of cancer. This sequence represents a prostate cancer
XX therapy associated cDNA. Note: The sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic
XX format directly from the US patent office at
XX seqdata.uspto.gov/sequence.html?docid=US20020192763
XX
XX
XX Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;
SQ
XX
XX Alignment Scores:
XX Pred. No.: 8 29e-70 Length: 1265
XX Score: 758.00 Matches: 146
XX Percent Similarity: 100.0% Conservative: 0
XX Best Local Similarity: 100.0% Mismatches: 0
XX Query Match: 100.0% Indels: 0
XX DB: 5 Gaps: 0
XX
XX US-10-726-093-10 (1-146) x ACAS9425 (1-1265)
QY 1 MetGluAaNGluLeuPheCysSerGlyValLeuValHisProGlnTTPValLeuSerAla 20
DB 40 ATGGAAACGAATTGTTCTGCTCGGCGCTGCTGGTGCATCCGCAATGGGTGCTGCACCC 99
QY 21 AlaHisCysPheGlnAaSerSerThrIleGlyLeuGlyLeuHisSerLeuGluAaSP 40
DB 100 GCACACTGTTTCCAAATCCTTCAACCATCGGCGCTGGGCTGCACAGTCTTAGGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAaSerLeuSerValArgHisProGlnTyrAsn 60
DB 160 CAAGAGCCAGGAGCCAGATGCTGAGAGCCAGCCCTCTCCGTACGGCACCCAGAGTACAAC 219
QY 61 ArgProLeuLeuAlaAaAspLeuMetLeuIleLysLeuAaSPGluSerValSerGluSer 80
DB 220 AGACCTTGTGCTGCTAACGACCTCATGCTCATCAAGTTGAGCAATCCGTGTCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAaSerGlnCysProThrAlaGlyAaSerCysLeu 100
DB 280 GACACCATCCGAGACATACGATTCCTTCTGCAATGCCCGGGGAACTTGGCTTC 339
QY 101 ValSerGlyTTPGlyLeuLeuAlaAaNGlyGluLeuThrGlyValCysLeuProSerSer 120

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```
Db 340 GTTCTGGCTGGGCTCTGCTGGCGAAGCTAGCTCAGCGGTGTGTCTGCTCTTCA 399
Qy 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlyCys 140
Db 400 AGGAGGTCCTCTGCTCCAGTCGGCGGGGGCTGACCCAGAGCTGCTCCAGGAGCAAGATGC 459
Qy 141 LeuProCysCysSerAla 146
Db 460 CTACCGTCTGTCAGTGGC 477

RESULT 12
AAS10167
ID AAS10167 standard; cDNA; 1265 BP.
XX AAS10167;
AC AAS10167;
XX 24-OCT-2001 (first entry)
DT
XX Human prostate tumour CDNA DE2.
DE
XX Human; prostate tumour protein; prostate cancer; ss.
KW
XX Homo sapiens.
OS
XX US6262245-B1.
XX 17-JUL-2001.
PD
XX 25-FEB-1998; 98US-00030607.
PF
XX 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC;
PI
XX WPI, 2001-440862/47.
DR
XX Novel polynucleotide encoding polypeptide comprising a portion of
PT prostate tumor protein useful for inhibiting development of prostate
PT cancer or for treating prostate cancer in a patient.
XX
XX Example 2; Col 169; 105pp; English.
XX
XX CC The sequence is a human prostate tumour CDNA which encodes a partial
CC tumour protein. The DNA is useful for inhibiting the development of
CC prostate cancer or for treating prostate cancer in a patient
XX
XX SQ Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;
SQ

Alignment Scores:
Pred. No.: 8 296-70 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
De: 5

US-10-726-093-10 (1-146) x AAS10167 (1-1265)
Qy 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
Db 40 ATGGAAAGCAATGTTCTGCTCGGGCGTCTGTGCATCCGACGGGTGCTGTCAGCC 99
Qy 21 AlaHisCysPheGlnAsnSerTrpThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
Db 100 GCACACTGTTTCCAGAACTCTACACATCGGGCTGGGCTGCACGCTCTTGAAGGCGAC 159
Qy 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTrpAsn 60
Db 160 CAAGACCCAGGAGCCAGATGTGTGAGGCGCAGCTCTCCGTACGGCAACCAGAGTAAAC 219
```

```
Qy 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
Db 220 AGACCCCTGCTGGCTAAAGACCTATGCTCATCAAGTTGAGCAATCCGTCTCCAGCT 279
Qy 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
Db 280 GACACATCCGGACATAGCATGCTTCCGAGGCCCTACCGCGGGAACTCTTGCTC 339
Qy 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
Db 340 GTTCTGGCTGGGCTGCTGCTGCGAAGCTCAGCGGTGTGTCTGCTCTTCA 399
Qy 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlyCys 140
Db 400 AGGAGGTCCTCTGCTCCAGTCGGCGGGGGCTGACCCAGAGCTGCTCCAGGAGCAATGC 459
Qy 141 LeuProCysCysSerAla 146
Db 460 CTACCGTCTGTCAGTGGC 477

RESULT 13
ABL94988
ID ABL94988 standard; cDNA; 1265 BP.
XX ABL94988;
AC ABL94988;
XX 19-JUL-2002 (first entry)
DT
XX Human P703P-DE2 CDNA sequence SEQ ID NO 173.
DE
XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
XX Homo sapiens.
OS
XX US2002022248-A1.
XX
XX 21-FEB-2002.
PD
XX
XX 12-JAN-2001; 2001US-00759143.
PF
XX 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 10-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00583793.
PR 27-JUN-2000; 2000US-00605783.
PR 10-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
XX
XX (XUJ/) XU J.
XX (DILL/) DILLON D C.
XX (MITC/) MITCHAM J L.
XX (HARL/) HARLOCKER S L.
XX (JIANG/) JIANG Y.
XX (KALO/) KALOS M D.
XX (FANG/) FANGER G R.
XX (RETT/) RETTER M W.
```

PA (STOL/) STOLK J. A.
 PA (DAYC/) DAY C. H.
 PA (VEDV/) VEDVICK T. S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S. X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y. A. W.
 PA (HEPL/) HEPLER W. T.
 PA (HEND/) HENDERSON R. A.
 XX
 PI Xu J., Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedrick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
 XX
 DR WPI; 2002-255649/30.
 XX
 PT New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer.
 XX
 PS Claim 1; SEQ ID NO 173; 87bp; English.
 XX
 CC The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a cDNA
 CC described in the invention

Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;

Alignment Scores:
 Pred. No.: 8,29e-70 Length: 1265
 Score: 758.00 Matches: 146
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 Gaps: 0

US-10-726-093-10 (1-146) x ABL94988 (1-1265)

QY 1 MetGluAnGluLeuPheCySerGlyValLeuValHisProGlnTrpValLeuSerAla 20
 DB 40 ATGGAAGAAAGATTGTTCTGCTCGGGCTCTGGTGCAATCCGACATGGGTCTGTACGCC 99
 QY 21 AlaHisCySPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaSP 40
 DB 100 GCACACTGTTCCAGAACTCTACACCAATCGGGCTGGGCTGCACAGTCTTAGCGCCGAC 159
 QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60
 DB 160 CAAGAGCCAGGAGCCAGATGATGTGAGGCGCAGCTCTCCGTACGGGACCCAGAGTACAAAC 219
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
 DB 220 AGACCTTGCTGCTGCTACGACCTCATGCTCAAGTTGAGCAATCCGTGCCGAGTCT 279
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCySProThrAlaGlyAsnSerCysLeu 100
 DB 280 GACACCATCCGAGGAGCATCGACTGCTTCGACAGTCCCTACCGCGGGAACCTTGCCCTC 339
 QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyValLeuThrGlyValCysLeuProSerSer 120
 DB 340 GTTTCGGCTGGGGGTGCTGGGGAAGGATGAGCTCAGCGGATGTGTCTGCTCTTCA 399
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlnCys 140
 DB 400 AGGAGGTCTCTGCCAGTCGGGGGGCTGACCCAGAGCTTGGCGTCCAGGACAGAAATCC 459
 QY 141 LeuProCySPCySerAla 146
 DB 460 CTACCGTCTCGCAGTCCG 477

RESULT 14
 ABS58697

ID ABS58697 standard; cDNA; 1265 BP.
 XX
 AC ABS58697;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Prostate tumour cDNA #168.
 XX
 KW Human; prostate tumour; immunotherapy; prostate cancer; gene; ss.
 OS Homo sapiens.
 XX
 XX US2002081580-A1.
 XX
 PD 27-JUN-2002.
 XX
 XX 25-FEB-1998; 98US-00030606.
 XX
 XX 25-FEB-1997; 97US-00806596.
 XX
 PR 01-AUG-1997; 97US-00804809.
 PR
 PR 09-FEB-1998; 98US-00020747.
 XX
 XX (XUJ/) XU J.
 PA (DILL/) DILLON D. C.
 XX
 PI Xu J., Dillon DC;
 XX
 XX WPI; 2002-607662/65.

Detecting prostate cancer comprises contacting a sample with an agent capable of binding to a polypeptide with an immunogenic portion of a prostate protein, oligonucleotide primers or a probe specific for DNA encoding the polypeptide.

Example 3; Page 88-89; 111pp; English.

The invention relates to a method of detecting prostate cancer by contacting a biological sample from a patient with: (a) a binding agent that binds to a polypeptide having an immunogenic portion of a prostate protein or its variant; (b) 2 oligonucleotide primers, where 1 of the oligonucleotides is specific for a DNA encoding the polypeptide of (a); or (c) an oligonucleotide probe specific for a DNA molecule encoding the polypeptide of (a). The method and polypeptides are useful for diagnosing, treating, particularly by immunotherapy, monitoring the progression, and inhibiting the development of prostate cancer in a patient. The polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. ABS58530-ABS58746 represent human prostate tumour cDNA sequences of the invention

Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;

Alignment Scores:
 Pred. No.: 8,29e-70 Length: 1265
 Score: 758.00 Matches: 146
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 Gaps: 0

US-10-726-093-10 (1-146) x ABS58697 (1-1265)

QY 1 MetGluAnGluLeuPheCySerGlyValLeuValHisProGlnTrpValLeuSerAla 20
 DB 40 ATGGAAGAAAGATTGTTCTGCTCGGGCTCTGGTGCAATCCGACATGGGTCTGTACGCC 99
 QY 21 AlaHisCySPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaSP 40
 DB 100 GCACACTGTTCCAGAACTCTTACACCAATCGGGCTGGGCTGCACAGTCTTAGAGCCGAC 159
 QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60
 DB 160 CAAGAGCCAGGAGCCAGATGATGTGAGGCGCAGCTCTCCGTACGGGACCCAGAGTACAAAC 219

QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLeuAspGluSerValSerGluSer 80
 DB 220 AGACCCCTTCCTCGCTACACCTCATGCTCATCAAGTTGAGCAATCCCTGTCGAGTCT 279
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
 DB 280 GACACCATCCGAGCATACGATTCCTGCGAGTCCCTACCGCGGGGAACCTCTGCTCA 339
 QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
 DB 340 GTTTCGCTGCGGTCTGCTGCGGAACGGTGAAGCTACCGGTGTGTGTCGCCCTTCA 399
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
 DB 400 AGAGAGTCTCTGCGCAGTCCGCGGGGCTGACCCAGAGCTCTGCTGCCAGCAGAAATGC 459
 QY 141 LeuProCysCysSerAla 146
 DB 460 CTACCGTCTGCGAGTCCG 477
 RESULT 15
 ACC95152
 ID ACC95152 standard; cDNA; 1265 BP.
 AC ACC95152;
 XX
 DT 28-AUG-2003 (first entry)
 XX
 DE Prostate tumour specific cDNA sequence SEQ ID 173.
 XX
 KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;
 XX
 KW Immune response; prostate cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200289747-A2.
 XX
 PD 14-NOV-2002.
 XX
 PF 09-MAY-2002; 2002MO-US014753.
 XX
 PR 09-MAY-2001; 2001US-00852911.
 PR 29-JUN-2001; 2001US-00895814.
 PR 10-DEC-2001; 2001US-00012896.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
 PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
 PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
 PI McNeill PD, Houghton RL, Vinals Y De BassolisC, Foy TW, Watanabe Y;
 PI Deng T;
 XX
 DR WPI; 2003-167130/16.
 XX
 PT New prostate-specific proteins and genes, useful in gene therapy,
 PT particularly for stimulating an immune response in a patient, or treating
 PT prostate cancer in a patient, as well as for diagnosing prostate cancer
 PT in a patient.
 XX
 PS Example 3; Page 353; 691pp; English.
 XX
 CC The present invention relates to novel prostate-specific proteins (PSP)
 CC and their coding sequences. The PSPs and their coding sequences are
 CC useful for stimulating an immune response in a patient, or for treating
 CC prostate cancer in a patient and for determining, detecting or diagnosing
 CC the presence of a cancer in a patient. The present sequence was used to
 CC illustrate the invention
 CC
 SQ Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;

Score: 758.00 Matches: 146
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 8 Gaps: 0
 US-10-726-093-10 (1-146) x ACC95152 (1-1265)
 QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
 DB 40 ATGGAACAAAGATTGTTCTGCTCGGCGCTCTGTCGATCCGACGTGGGTCTGTACGC 99
 QY 21 AlaHisCysPheGlnAsnSerThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
 DB 100 GACACTGTTTCCAAACTCTTACACCATCGGGCTGGGCTGCCTCACAAGTCTTAGGCCGAC 159
 QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTrpAsn 60
 DB 160 CAAGAGCCAGGAGCCAGATGGTGGAGGCCAGCTCTCCGTACGGCACCAGAGTACAAAC 219
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLeuAspGluSerValSerGluSer 80
 DB 220 AGACCCCTTCCTCGCTACACCTCATGCTCATCAAGTTGAGCAATCCCTGTCGAGTCT 279
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
 DB 280 GACACCATCCGAGCATACGATTCCTGCGAGTCCCTACCGCGGGGAACCTCTGCTCA 339
 QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
 DB 340 GTTTCGCTGCGGTCTGCTGCGGAACGGTGAAGCTACCGGTGTGTGTCGCCCTTCA 399
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
 DB 400 AGAGAGTCTCTGCGCAGTCCGCGGGGCTGACCCAGAGCTCTGCTGCCAGCAGAAATGC 459
 QY 141 LeuProCysCysSerAla 146
 DB 460 CTACCGTCTGCGAGTCCG 477

Search completed: August 28, 2006, 18:23:29
 Job time : 527 secs

Alignment Scores: 8.29e-70 Length: 1265
 Pred. No.: